

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2005, 15:46:34 ; Search time 20.7308 Seconds
(without alignments)
50.412 Million cell updates/sec

Title: US-09-831-253F-2
Perfect score: 89
Sequence: 1 FCLGPCPYWISLDT 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	23	1	US-08-486-057B-26
2	89	100.0	23	2	US-08-789-588-26
3	89	100.0	25	4	US-09-095-637D-4
4	89	100.0	51	6	5168051-4
5	89	100.0	51	6	5168051-4
6	89	100.0	60	3	US-09-363-939A-122
7	89	100.0	60	4	US-09-791-301-122
8	89	100.0	70	4	US-08-848-664A-9
9	89	100.0	98	3	US-08-478-097A-1
10	89	100.0	98	3	US-08-931-858E-150
11	89	100.0	98	3	US-08-981-739-150
12	89	100.0	98	4	US-09-128-026-150
13	89	100.0	98	4	US-09-496-398-1
14	89	100.0	98	4	US-09-374-958C-40
15	89	100.0	98	4	US-09-374-958C-40
16	89	100.0	98	4	US-09-220-527-150
17	89	100.0	98	4	US-09-220-527-150
18	89	100.0	112	1	US-07-979-441-1
19	89	100.0	112	1	US-08-197-792-36
20	89	100.0	112	1	US-08-486-057B-41
21	89	100.0	112	1	US-08-459-850-36
22	89	100.0	112	1	US-08-459-214-36
23	89	100.0	112	1	US-08-470-837-30
24	89	100.0	112	2	US-08-789-588-41
25	89	100.0	112	2	US-08-410-573-1
26	89	100.0	112	3	US-09-123-233-2
27	89	100.0	112	3	US-08-927-433-5

28	89	100.0	112	3	US-08-868-452-30	Sequence 30, Appl
29	89	100.0	112	4	US-09-095-637D-1	Sequence 1, Appl
30	89	100.0	112	5	PCT-US93-03068-1	Sequence 1, Appl
31	89	100.0	114	1	US-08-481-377-23	Sequence 23, Appl
32	89	100.0	114	2	US-08-491-835-21	Sequence 21, Appl
33	89	100.0	114	3	US-09-153-733A-23	Sequence 23, Appl
34	89	100.0	114	3	US-08-946-092A-21	Sequence 21, Appl
35	89	100.0	114	3	US-09-172-062-21	Sequence 21, Appl
36	89	100.0	114	3	US-08-624-635-22	Sequence 22, Appl
37	89	100.0	114	3	US-09-301-520D-21	Sequence 21, Appl
38	89	100.0	114	3	US-09-389-705-23	Sequence 23, Appl
39	89	100.0	114	5	PCT-US94-00666-23	Sequence 23, Appl
40	89	100.0	114	5	PCT-US94-00685-21	Sequence 21, Appl
41	89	100.0	115	1	US-08-581-5529B-19	Sequence 19, Appl
42	89	100.0	115	1	US-08-455-559-25	Sequence 25, Appl
43	89	100.0	115	2	US-08-525-596B-29	Sequence 29, Appl
44	89	100.0	115	2	US-08-581-528A-19	Sequence 19, Appl
45	89	100.0	115	3	US-09-097-616-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-486-057B-26
Sequence 26, Application US/08486057B
Patent No. 5650494
GENERAL INFORMATION:
APPLICANT: Cerletti, Nico
APPLICANT: McMaster, Gary K.
APPLICANT: Cox, David
APPLICANT: Schmitz, Albert
APPLICANT: Meyhack, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry P. No. 5650494k
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,057B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502
FILING DATE: 03-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: No. 5650494k, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 4-17861/*Cont3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:

5168051-4

Query Match 100.0%; Score 89; DB 6; Length 51;

Best Local Similarity 100.0%; Pred. No. 4.1e-05; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14

Db 34 FCLGPCPYIWSLDT 47

RESULT 6

US-09-363-939A-122

Sequence 122, Application US/09363939A

Patent No. 6346611

GENERAL INFORMATION:

APPLICANT: Pagratia, Nikos

APPLICANT: Lochrie, Michael

TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and

TITLE OF INVENTION: Inhibitors

FILE REFERENCE: NEX87

CURRENT APPLICATION NUMBER: US/09/363,939A

CURRENT FILING DATE: 1999-07-29

PRIOR APPLICATION NUMBER: 09/046,247

PRIOR FILING DATE: 1998-03-23

PRIOR APPLICATION NUMBER: 08/458,424

PRIOR FILING DATE: 1995-06-02

PRIOR APPLICATION NUMBER: 07/714,131

PRIOR FILING DATE: 1991-06-10

PRIOR APPLICATION NUMBER: 07/931,473

PRIOR FILING DATE: 1992-08-17

PRIOR APPLICATION NUMBER: 07/964,624

PRIOR FILING DATE: 1992-10-21

PRIOR APPLICATION NUMBER: 08/117,991

PRIOR FILING DATE: 1993-09-08

PRIOR APPLICATION NUMBER: 07/536,428

PRIOR FILING DATE: 1990-06-11

NUMBER OF SEQ ID NOS: 216

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 122

LENGTH: 60

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-363-939A-122

Query Match 100.0%; Score 89; DB 3; Length 60;

Best Local Similarity 100.0%; Pred. No. 4.7e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14

Db 43 FCLGPCPYIWSLDT 56

RESULT 7

US-09-791-301-122

Sequence 122, Application US/09791301

Patent No. 6713616

GENERAL INFORMATION:

APPLICANT: Pagratia, Nikos

APPLICANT: Lochrie, Michael

TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and

TITLE OF INVENTION: Inhibitors

FILE REFERENCE: NEX 87/C

CURRENT APPLICATION NUMBER: US/09/791,301

CURRENT FILING DATE: 2001-02-23

PRIOR APPLICATION NUMBER: 09/046,247

PRIOR FILING DATE: 1998-03-23

PRIOR APPLICATION NUMBER: 08/458,424

PRIOR FILING DATE: 1995-06-02

PRIOR APPLICATION NUMBER: 07/714,131

PRIOR FILING DATE: 1991-06-10

PRIOR APPLICATION NUMBER: 07/931,473

PRIOR FILING DATE: 1992-08-17

PRIOR APPLICATION NUMBER: 07/964,624

PRIOR FILING DATE: 1992-10-21

PRIOR APPLICATION NUMBER: 08/117,991

PRIOR FILING DATE: 1993-09-08

PRIOR APPLICATION NUMBER: 07/536,428

PRIOR FILING DATE: 1990-06-11

PRIOR APPLICATION NUMBER: 09/363,939

PRIOR FILING DATE: 1999-07-29

NUMBER OF SEQ ID NOS: 216

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 122

LENGTH: 60

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-791-301-122

Query Match 100.0%; Score 89; DB 4; Length 60;

Best Local Similarity 100.0%; Pred. No. 4.7e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14

Db 43 FCLGPCPYIWSLDT 56

RESULT 8

US-09-848-664A-9

Sequence 9, Application US/09848664A

Patent No. 6723344

GENERAL INFORMATION:

APPLICANT: Sakiyama-Bibert, Shelly E.

APPLICANT: Hubbard, Jeffrey A.

TITLE OF INVENTION: Controlled Release of No. 6723344-Heparin Binding Growth

TITLE OF INVENTION: Factors from Heparin Containing Matrices

FILE REFERENCE: ETH 108

CURRENT APPLICATION NUMBER: US/09/848,664A

CURRENT FILING DATE: 2001-05-03

PRIOR APPLICATION NUMBER: US/09/298,084A

PRIOR FILING DATE: 1999-04-22

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 9

LENGTH: 70

TYPE: PRT

ORGANISM: Homo sapiens

US-09-848-664A-9

Query Match 100.0%; Score 89; DB 4; Length 70;

Best Local Similarity 100.0%; Pred. No. 5.4e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14

Db 43 FCLGPCPYIWSLDT 56

RESULT 9

US-08-478-097A-1

Sequence 1, Application US/08478097A

Patent No. 6040431

GENERAL INFORMATION:

APPLICANT: KECK, PETER

APPLICANT: SMART, JOHN

TITLE OF INVENTION: SINGLE-CHAIN ANALOGS OF TGF-B

TITLE OF INVENTION: SUPERFAMILY (MORPHONS)
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT, LLP
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,097A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-080
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..98
OTHER INFORMATION: /note= "TGF-B1 SEQUENCE"
US-08-478-097A-1
Query Match 100.0%; Score 89; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FCLGPCPYIWSLDT 14
Db 29 FCLGPCPYIWSLDT 42
RESULT 10
US-08-931-858E-150
Sequence 150, Application US/08931858E
Patent No. 6222022
GENERAL INFORMATION:
APPLICANT: JOHNSON, EUGENE M
APPLICANT: MILBRANDT, JEFFREY D
APPLICANT: KOTZBAUER, PAUL T
APPLICANT: LAMPE, PATRICIA A
APPLICANT: KLEIN, ROBERT
APPLICANT: DESAUVAGE, FRED
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,858E
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971486
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-931-858E-150
Query Match 100.0%; Score 89; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FCLGPCPYIWSLDT 14
Db 29 FCLGPCPYIWSLDT 42
RESULT 11
US-08-981-739-150
Sequence 150, Application US/08981739
Patent No. 6232449
GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: LAMPE, PATRICIA A.
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,739
FILING DATE: 31-Aug-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/03461
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976163
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 150:
US-08-981-739-150

Query Match 100.0%; Score 89; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGCPYIWSLDT 14
|||||
Db 29 FCLGCPYIWSLDT 42

RESULT 12
US-09-128-026-150
; Sequence 150, Application US/09128026
; Patent No. 6403335
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOMEL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/128,026
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 976163
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-128-026-150

Query Match 100.0%; Score 89; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGCPYIWSLDT 14
|||||
Db 29 FCLGCPYIWSLDT 42

RESULT 13
US-09-496-398-1
; Sequence 1, Application US/09496398
; Patent No. 6479643
; GENERAL INFORMATION:
; APPLICANT: KECK, PETER
; APPLICANT: SMART, JOHN
; TITLE OF INVENTION: SINGLE CHAIN ANALOGS OF TGF-B
; TITLE OF INVENTION: SUPERFAMILY (MORPHONS)

NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HURWITZ &
ADDRESSEE: THIREAULT, LLP
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/496,398
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,097
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STK-059CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..98
OTHER INFORMATION: /note="TGF-B1 SEQUENCE"
US-09-496-398-1

Query Match 100.0%; Score 89; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGCPYIWSLDT 14
|||||
Db 29 FCLGCPYIWSLDT 42

RESULT 14
US-09-220-616-150
; Sequence 150, Application US/09220616
; Patent No. 6645937
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOMEL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/220,616
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,739
; FILING DATE: 31-Aug-1998
; APPLICATION NUMBER: PCT/US97/03461
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE//DOCKET NUMBER: 976163
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-220-616-150

```

```

Query Match          100.0%; Score 89; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 FCLGPCPYIWSLDT 14
        |||||
Db      29 FCLGPCPYIWSLDT 42

```

```

RESULT 15
US-09-374-958C-40
; Sequence 40, Application US/09374958C
; Patent No. 6677432
; GENERAL INFORMATION:
; APPLICANT: Stryker Corporation
; TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, Including
; FILE REFERENCE: STR-076
; CURRENT APPLICATION NUMBER: US/09/374,958C
; CURRENT FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 40
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TGF-Beta1
US-09-374-958C-40

```

```

Query Match          100.0%; Score 89; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 FCLGPCPYIWSLDT 14
        |||||
Db      29 FCLGPCPYIWSLDT 42

```

```

Search completed: June 14, 2005, 16:10:14
Job time : 20.7308 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2005, 15:46:34 ; Search time 22.2115 Seconds
(without alignments)
50.412 Million cell updates/sec

Title: US-09-831-253f-1
Perfect score: 96
Sequence: 1 HANFCLGRCFYWSL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	23	1	US-08-486-057B-26
2	96	100.0	23	2	US-08-789-588-26
3	96	100.0	51	6	5168051-4
4	96	100.0	51	6	5168051-4
5	96	100.0	60	3	US-09-363-939A-122
6	96	100.0	60	4	US-09-791-301-122
7	96	100.0	70	4	US-09-848-664A-9
8	96	100.0	98	3	US-08-478-097A-1
9	96	100.0	98	3	US-08-931-858B-150
10	96	100.0	98	3	US-08-981-739-150
11	96	100.0	98	4	US-09-128-028-150
12	96	100.0	98	4	US-09-436-398-1
13	96	100.0	98	4	US-09-220-616-150
14	96	100.0	98	4	US-09-374-958C-40
15	96	100.0	98	4	US-09-220-527-150
16	96	100.0	98	4	US-09-220-407-150
17	96	100.0	112	1	US-07-979-441-1
18	96	100.0	112	1	US-08-197-792-36
19	96	100.0	112	1	US-08-486-057B-41
20	96	100.0	112	1	US-08-486-850-36
21	96	100.0	112	1	US-08-459-214-36
22	96	100.0	112	1	US-08-470-837-30
23	96	100.0	112	1	US-08-789-588-41
24	96	100.0	112	2	US-08-410-573-1
25	96	100.0	112	2	US-09-123-233-2
26	96	100.0	112	3	US-08-927-433-5
27	96	100.0	112	3	US-08-868-453-30

28	96	100.0	112	4	US-09-095-637D-1	Sequence 1, Appl
29	96	100.0	112	5	PCT-US93-03068-1	Sequence 1, Appl
30	96	100.0	114	1	US-08-481-377-23	Sequence 23, Appl
31	96	100.0	114	2	US-08-491-835-21	Sequence 21, Appl
32	96	100.0	114	3	US-09-153-733A-23	Sequence 23, Appl
33	96	100.0	114	3	US-08-946-092A-21	Sequence 21, Appl
34	96	100.0	114	3	US-09-172-062-21	Sequence 21, Appl
35	96	100.0	114	3	US-08-624-635-22	Sequence 22, Appl
36	96	100.0	114	3	US-09-301-530D-21	Sequence 21, Appl
37	96	100.0	114	3	US-09-389-705-23	Sequence 23, Appl
38	96	100.0	114	5	PCT-US94-00666-23	Sequence 23, Appl
39	96	100.0	114	5	PCT-US94-00685-21	Sequence 21, Appl
40	96	100.0	115	1	US-08-581-529B-19	Sequence 19, Appl
41	96	100.0	115	1	US-08-455-559-25	Sequence 25, Appl
42	96	100.0	115	2	US-08-525-596B-29	Sequence 29, Appl
43	96	100.0	115	2	US-08-581-528A-19	Sequence 19, Appl
44	96	100.0	115	3	US-09-097-616-19	Sequence 19, Appl
45	96	100.0	115	3	US-09-177-860A-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-486-057B-26
Sequence 26, Application US/08486057B
Patent No. 5650494
GENERAL INFORMATION:
APPLICANT: Cerletti, Nico
APPLICANT: McMaster, Gary K.
APPLICANT: Cox, David
APPLICANT: Schmitz, Albert
APPLICANT: Meyhack, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry P. No. 5650494k
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,057B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502
FILING DATE: 03-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: No. 5650494k, Henry P.
REGISTRATION NUMBER: 33200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-486-057B-26

Query Match 100.0%; Score 96; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1,4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWSL 15
|||
3 HANFCLGCPYIWSL 17

RESULT 2
US-08-789-588-26

Sequence 26, Application US/08789588
Patent No. 5922846

GENERAL INFORMATION:

APPLICANT: Cellecti, Nicco
APPLICANT: McMaster, Gary K.

APPLICANT: Cox, David

APPLICANT: Schmitz, Albert

APPLICANT: Meyhack, Bernd

TITLE OF INVENTION: Process for Refolding Recombinantly

TITLE OF INVENTION: Produced TGF-beta-like Proteins

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Henry P. No. 5922846ak

STREET: 520 White Plains Road, P.O. Box 2005

CITY: Tarrytown

STATE: New York

COUNTRY: U.S.A.

ZIP: 10591-9005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/789,588

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/486,057

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/201,703

FILING DATE: 25-FEB-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/960,309

FILING DATE: 13-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/621,502

FILING DATE: 03-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 8927546.5

FILING DATE: 06-DEC-1989

ATTORNEY/AGENT INFORMATION:

NAME: No. 5922846ak, Henry P.

REGISTRATION NUMBER: 33200

REFERENCE/DOCKET NUMBER: 4-17861/-/Cont3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 277-5110

TELEFAX: (908) 277-4306

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-789-588-26

Query Match 100.0%; Score 96; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1,4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWSL 15
|||
3 HANFCLGCPYIWSL 17

RESULT 3
5168051-4

Patent No. 5168051

APPLICANT: DERYNCK, RIK M.A.;GOEDEL, DAVID V.

TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES

NUMBER OF SEQUENCES: 21

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/389,929

FILING DATE: 04-AUG-1989

SEQ ID NO:4:

LENGTH: 51

5168051-4

Query Match 100.0%; Score 96; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 2,8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWSL 15
|||
31 HANFCLGCPYIWSL 45

RESULT 4
5168051-4

Patent No. 5168051

APPLICANT: DERYNCK, RIK M.A.;GOEDEL, DAVID V.

TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES

NUMBER OF SEQUENCES: 21

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/389,929

FILING DATE: 04-AUG-1989

SEQ ID NO:4:

LENGTH: 51

5168051-4

Query Match 100.0%; Score 96; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 2,8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWSL 15
|||
31 HANFCLGCPYIWSL 45

RESULT 5
US-09-363-939A-122

Sequence 122, Application US/09363939A

Patent No. 6346611

GENERAL INFORMATION:

APPLICANT: Pagratlis, Nikos

APPLICANT: Lochrie, Michael

APPLICANT: Gold, Larry

TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and

TITLE OF INVENTION: Inhibitors

FILE REFERENCE: NEX87

CURRENT APPLICATION NUMBER: US/09/363,939A

CURRENT FILING DATE: 1999-07-29

PRIOR APPLICATION NUMBER: 09/046,247

PRIOR FILING DATE: 1998-03-23

PRIOR APPLICATION NUMBER: 08/458,424

PRIOR FILING DATE: 1995-06-02

PRIOR APPLICATION NUMBER: 07/714,131

PRIOR FILING DATE: 1991-06-10
PRIOR APPLICATION NUMBER: 07/931,473
PRIOR FILING DATE: 1992-08-17
PRIOR APPLICATION NUMBER: 07/964,624
PRIOR FILING DATE: 1992-10-21
PRIOR APPLICATION NUMBER: 08/117,991
PRIOR FILING DATE: 1993-09-08
PRIOR APPLICATION NUMBER: 07/536,428
PRIOR FILING DATE: 1990-06-11
NUMBER OF SEQ ID NOS: 216
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 122
LENGTH: 60
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-363-939A-122

Query Match 100.0%; Score 96; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGCPYIWSL 15
Db 40 HANFCLGCPYIWSL 54

RESULT 6
US-09-791-301-122
Sequence 122, Application US/09791301
Patent No. 6713616
GENERAL INFORMATION:
APPLICANT: Pagratlis, Nikos
APPLICANT: Lochrie, Michael
APPLICANT: Gold, Larry
TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
TITLE OF INVENTION: Inhibitors
FILE REFERENCE: NEX 87/C
CURRENT APPLICATION NUMBER: US/09/791,301
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 09/046,247
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: 08/458,424
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: 07/714,131
PRIOR FILING DATE: 1991-06-10
PRIOR APPLICATION NUMBER: 07/931,473
PRIOR FILING DATE: 1992-08-17
PRIOR APPLICATION NUMBER: 07/964,624
PRIOR FILING DATE: 1992-10-21
PRIOR APPLICATION NUMBER: 08/117,991
PRIOR FILING DATE: 1993-09-08
PRIOR APPLICATION NUMBER: 07/536,428
PRIOR FILING DATE: 1990-06-11
PRIOR APPLICATION NUMBER: 09/363,939
PRIOR FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 216
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 122
LENGTH: 60
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-791-301-122

Query Match 100.0%; Score 96; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGCPYIWSL 15
Db 40 HANFCLGCPYIWSL 54

RESULT 7
US-09-848-664A-9
Sequence 9, Application US/09848664A
Patent No. 6723344
GENERAL INFORMATION:
APPLICANT: Sakiyama-Elbert, Shelly E.
APPLICANT: Hubbell, Jeffrey A.
TITLE OF INVENTION: Controlled Release of No. 6723344-Heparin Binding Growth
FILE REFERENCE: ETH 108
CURRENT APPLICATION NUMBER: US/09/848,664A
CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: US/09/298,084A
PRIOR FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 70
TYPE: PRT
ORGANISM: Homo sapiens
US-09-848-664A-9

Query Match 100.0%; Score 96; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGCPYIWSL 15
Db 40 HANFCLGCPYIWSL 54

RESULT 8
US-08-478-097A-1
Sequence 1, Application US/08478097A
Patent No. 6040431
GENERAL INFORMATION:
APPLICANT: KECK, PETER
APPLICANT: SMART, JOHN
TITLE OF INVENTION: SINGLE-CHAIN ANALOGS OF TGF-B
TITLE OF INVENTION: SUPERFAMILY (MORPHONS)
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HURWITZ &
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,097A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-080
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..98
OTHER INFORMATION: /note="TGF-B1 SEQUENCE"
US-08-478-097A-1

Query Match 100.0%; Score 96; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGPCPYIWSL 15
DB 26 HANFCLGPCPYIWSL 40

RESULT 9
US-08-931-858E-150
Sequence 150, Application US/08931858E
Patent No. 6222022
GENERAL INFORMATION:
APPLICANT: JOHNSON, EUGENE M
APPLICANT: MILBRANDT, JEFFREY D
APPLICANT: KOTZBAUER, PAUL T
APPLICANT: LAMPE, PATRICIA A
APPLICANT: KLEIN, ROBERT
APPLICANT: DESAUVAGE, FRED
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,858E
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971486
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-931-858E-150

Query Match 100.0%; Score 96; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGPCPYIWSL 15
DB 26 HANFCLGPCPYIWSL 40

RESULT 10
US-08-981-739-150
Sequence 150, Application US/08981739
Patent No. 6232449
GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: LAMPE, PATRICIA A.
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,739
FILING DATE: 31-Aug-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/03461
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976163
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 150:
US-08-981-739-150

Query Match 100.0%; Score 96; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGPCPYIWSL 15
DB 26 HANFCLGPCPYIWSL 40

RESULT 11
US-09-128-026-150
Sequence 150, Application US/09128026
Patent No. 6403335
GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: LAMPE, PATRICIA A.
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US

```

; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/128,026
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 976163
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-128-026-150

Query Match      100.0%; Score 96; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HANFCLGPCPYIWSL 15
      |||||
Db      26 HANFCLGPCPYIWSL 40

RESULT 12
US-09-496-398-1
; Sequence 1, Application US/09496398
; Patent No. 6479643
; GENERAL INFORMATION:
; APPLICANT: KECK, PETER
; APPLICANT: SMART, JOHN
; TITLE OF INVENTION: SINGLE CHAIN ANALOGS OF TGF-B
; TITLE OF INVENTION: SUPERFAMILY (MORPHONS)
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT, LLP
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/496,398
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,097
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: BITCHER ESO, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: STK-059CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7000
; TELEFAX: 617-248-7100
```

```

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..98
; OTHER INFORMATION: /note="TGF-B1 SEQUENCE"
; US-09-496-398-1

Query Match      100.0%; Score 96; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HANFCLGPCPYIWSL 15
      |||||
Db      26 HANFCLGPCPYIWSL 40

RESULT 13
US-09-220-616-150
; Sequence 150, Application US/09220616
; Patent No. 6645937
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/220,616
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,739
; FILING DATE: 31-Aug-1998
; APPLICATION NUMBER: PCT/US97/03461
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 976163
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-220-616-150

Query Match      100.0%; Score 96; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 HANFCLGCPYIWSL 15
|||
Db 26 HANFCLGCPYIWSL 40

RESULT 14
US-09-374-958C-40
Sequence 40, Application US/09374958C
Patent No. 6677432
GENERAL INFORMATION:
APPLICANT: Stryker Corporation
TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, Including
FILE REFERENCE: STK-076
CURRENT APPLICATION NUMBER: US/09/374,958C
CURRENT FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PatentIn version 2.0
SEQ ID NO 40
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: TGF-Beta1
US-09-374-958C-40

Query Match 100.0%; Score 96; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. NO. 5.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWSL 15
|||
Db 26 HANFCLGCPYIWSL 40

RESULT 15
US-09-220-527-150
Sequence 150, Application US/09220527
Patent No. 6692943
GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
MILBRANDT, JEFFREY D.
KOTZBAUER, PAUL T.
LAMPE, PATRICIA A.
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/220,527
FILING DATE: 24-Dec-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/981,739
FILING DATE: 31-Aug-1998
APPLICATION NUMBER: PCT/US97/03461
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976163
TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 150:
US-09-220-527-150

Query Match 100.0%; Score 96; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. NO. 5.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWSL 15
|||
Db 26 HANFCLGCPYIWSL 40

Search completed: June 14, 2005, 16:10:14
Job time : 23.2115 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2005, 15:29:15 ; Search time 85.9615 Seconds
(without alignments)
67.488 Million cell updates/sec

Title: US-09-831-253f-1
Perfect score: 96
Sequence: 1 HANCLGPCPYTWSL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	15	3	AAV92965 Transform
2	96	100.0	15	3	AAV92945 Transform
3	96	100.0	23	3	AAV92983 Transform
4	96	100.0	23	3	AAV92954 Transform
5	96	100.0	50	2	AAV90828 Pre-trans
6	96	100.0	51	2	AAV90475 Sequence
7	96	100.0	51	4	AAV78788 Human tra
8	96	100.0	51	4	AAV43879 Peptide #
9	96	100.0	51	4	AAV37799 Peptide #
10	96	100.0	51	4	AAV7605 Human Don
11	96	100.0	51	5	ABG46640 Human pep
12	96	100.0	60	4	AAV68685 Human TGF
13	96	100.0	62	2	AAV30331 Fragment
14	96	100.0	65	2	AAV22135 PDGF subu
15	96	100.0	98	2	AAV16697 MO9914235
16	96	100.0	98	3	AAV92854 TGF-beta
17	96	100.0	98	3	AAV09519 Human TGF
18	96	100.0	98	3	AAV02785 Human TGF
19	96	100.0	112	2	AAV08142 Platelet-
20	96	100.0	112	2	AAV04076 Sequence
21	96	100.0	112	2	AAV12402 Transform
22	96	100.0	112	2	AAV22134 PDGF subu
23	96	100.0	112	2	AAV43263 TGF-beta.
24	96	100.0	112	2	AAV42311 Recombina
25	96	100.0	112	2	AAV92773 Human TGF

26	96	100.0	112	2	AAV91956 Human tra
27	96	100.0	112	2	AAV08173 TGF-beta1
28	96	100.0	112	2	AAV78781 Human tra
29	96	100.0	112	2	AAV97091 The matur
30	96	100.0	112	2	AAV08299 Human gro
31	96	100.0	112	2	AAV84207 Transform
32	96	100.0	112	3	AAV67950 Human tra
33	96	100.0	112	3	AAV92010 Human tra
34	96	100.0	112	2	AAV35937 TGF-beta
35	96	100.0	112	5	AAV51939 Human TGF
36	96	100.0	112	6	AAV08656 Human tra
37	96	100.0	112	8	AAV11598 Human bon
38	96	100.0	112	8	AAV79530 Human tra
39	96	100.0	114	2	AAV39638 Human tra
40	96	100.0	115	4	AAV73204 TGF-beta1
41	96	100.0	115	6	AAV76033 Human TGF
42	96	100.0	118	2	AAV08176 TGF-beta
43	96	100.0	120	8	AAV17006 Porcine T
44	96	100.0	120	8	AAV17010 Porcine T
45	96	100.0	122	2	AAV08181 TGF-beta

ALIGNMENTS

RESULT 1	AAV92965	standard; peptide, 15 AA.
ID	AAV92965	
AC	AAV92965;	
XX		
XX		
XX	08-NOV-2000	(first entry)
DT		
XX		
XX		
DE	Transforming growth factor inhibitory peptide p11.	
XX		
XX	Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;	
KW	competitive inhibition; collagen synthesis stimulation inhibitor; liver;	
KW	extracellular matrix degradation inhibitor; mimotope; cirrhosis.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200031135-A1.	
XX		
PD	02-JUN-2000.	
XX		
PF	23-NOV-1999;	99WO-ES000375.
XX		
PR	24-NOV-1998;	98ES-00002465.
XX		
PA	(CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.	
XX		
XX	Ezquerro Saenz JI, Lasarte Sagastibelza JI, Prieto Valtuena J;	
PI	Borras Cuesta F;	
XX		
DR	WPI, 2000-411935/35.	
XX		
PT	Peptides that antagonize binding of transforming growth factor beta1,	
PT	useful for treatment of liver disease, especially cirrhosis, are partial	
XX	sequences of the factor or its receptors.	
PS		
XX	Disclosure; Page 22; 86pp; Spanish.	
CC	The invention relates to synthetic peptides that antagonise the binding	
CC	of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor in	
CC	vivo which have partial amino acid sequences identical, or similar, with	
CC	those of TGF-beta1 and/or its receptors. Peptides AAV92945-Y93133 represent	
CC	examples of the peptides of the invention. The peptides act by	
CC	competitive inhibition of the binding of TGF-beta1 to its receptors, e.g.	
CC	they are inhibitors of stimulation of collagen synthesis in liver cells	
CC	and inhibitors of synthesis of proteolytic enzymes able to degrade the	
CC	extracellular matrix. The peptides, their mimetopes and/or DNA (or	
CC	expression systems) encoding the peptides are used for treatment of liver	
CC	disease, specifically cirrhosis	

XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 96; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGPCPYIWSL 15
DB 1 HANFCLGPCPYIWSL 15

RESULT 2

AA92945
ID AA92945 standard; peptide; 15 AA.

AC AA92945;

DT 08-NOV-2000 (first entry)

DE Transforming growth factor inhibitory peptide #1.

KM Hepatotropic; antagonist; transforming growth factor betaf; TGF-b1;
KM competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KM extracellular matrix degradation inhibitor; mimotope; cirrhosis.

OS Homo sapiens.

PN WO200031135-A1.

PD 02-JUN-2000.

PF 23-NOV-1999; 99WO-ES000375.

PR 24-NOV-1998; 98ES-00002465.

PA (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.

PI Ezquerro Saenz JI, Lasaarte Sagastibelza JI, Prieto Valtuena JI;

PI Borras Cuesta F;

XX WPI; 2000-411935/35.

PT Peptides that antagonize binding of transforming growth factor betaf,
PT useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.

PS Claim 2; Page 80; 86pp; Spanish.

CC The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor betaf (TGF-b1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-b1 and/or its receptors. Peptides AA92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis

CC
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 96; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGPCPYIWSL 15
DB 1 HANFCLGPCPYIWSL 15

RESULT 3

AA92983
ID AA92983 standard; peptide; 23 AA.

AC AA92983;

DT 08-NOV-2000 (first entry)

DE Transforming growth factor inhibitory peptide P29.

KM Hepatotropic; antagonist; transforming growth factor betaf; TGF-b1;
KM competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KM extracellular matrix degradation inhibitor; mimotope; cirrhosis.

OS Homo sapiens.

PN WO200031135-A1.

PD 02-JUN-2000.

PF 23-NOV-1999; 99WO-ES000375.

PR 24-NOV-1998; 98ES-00002465.

PA (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.

PI Ezquerro Saenz JI, Lasaarte Sagastibelza JI, Prieto Valtuena JI;

PI Borras Cuesta F;

XX WPI; 2000-411935/35.

PT Peptides that antagonize binding of transforming growth factor betaf,
PT useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.

PS Disclosure; Page 24; 86pp; Spanish.

CC The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor betaf (TGF-b1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-b1 and/or its receptors. Peptides AA92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis

CC
XX
SQ Sequence 23 AA;

Query Match 100.0%; Score 96; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGPCPYIWSL 15
DB 7 HANFCLGPCPYIWSL 21

RESULT 4

AA92954
ID AA92954 standard; peptide; 23 AA.

AC AA92954;

DT 08-NOV-2000 (first entry)

DE Transforming growth factor inhibitory peptide #10.

KM Hepatotropic; antagonist; transforming growth factor betaf; TGF-b1;
KM competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KM extracellular matrix degradation inhibitor; mimotope; cirrhosis.

OS	Homo sapiens.
PN	WO200031135-A1.
PD	02-JUN-2000.
PF	23-NOV-1999; 99WO-ES000375.
PR	24-NOV-1998; 98ES-00002465.
PA	(CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.
PI	Ezquerro Saenz J ^U , Lasarte Sagasibelza J ^J , Prieto Valtuena J;
PI	Borras Cueta F;
DR	WPI, 2000-411935/35.
XX	
PT	Peptides that antagonize binding of transforming growth factor beta1,
PT	useful for treatment of liver disease, especially cirrhosis, are partial
PT	sequences of the factor or its receptors.
PS	Claim 11; Page 82; 86pp; Spanish.
XX	
CC	The invention relates to synthetic peptides that antagonise the binding
CC	of transforming growth (TGF) factor beta1 (TGF- β 1) to its receptor in
CC	vivo which have partial amino acid sequences identical, or similar, with
CC	those of TGF- β 1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC	examples of the peptides of the invention. The peptides act by
CC	competitive inhibition of the binding of TGF- β 1 to its receptors, e.g.
CC	they are inhibitors of stimulation of collagen synthesis in liver cells
CC	and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC	extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC	expression systems) encoding the peptides are used for treatment of liver
CC	disease, specifically cirrhosis
XX	
SO	Sequence 23 AA;
Qy	1 HANPCLGPCPYIWSL 15
Db	7 HANPCLGPCPYIWSL 21
Query Match	100.0%; Score 96; DB 3; Length 23;
Best Local Similarity	100.0%; Pred. No. 2.9e-06;
Matches 15; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
RESULT 5	
ID	AAR90828 standard; peptide; 50 AA.
AC	AAR90828;
XX	
DT	25-MAR-2003 (revised)
DT	25-JAN-1980 (first entry)
XX	
DE	Pre-transforming growth factor beta 1 residues 252 to 302.
XX	
XX	transforming growth factor beta 1, wound healing; recombinant production.
OS	Homo sapiens.
PN	US5482851-A.
PD	09-JAN-1996.
PF	05-NOV-1993; 93US-00147364.
PR	22-MAR-1985; 85US-00715142.
PR	13-MAR-1987; 87US-00025423.
PR	04-AUG-1989; 89US-00389929.
PR	04-MAR-1992; 92US-00845893.
PA	(GETH) GENENTECH INC.

```

XX XX Goeddel DV, Derynck RMA;
PI XX
DR DR WPI, 1996-076891/08.
XX N-PSDB; AAT15721.
XX
PT PT New recombinant human transforming growth factor-beta prods. - produced
PR using Chinese hamster ovary cells, for use in diagnostic applications or
PT in therapy.
XX
PS Example 2; Fig 2; 26pp; English.
XX
CC The transforming growth factor (TGF) beta 1 exon (residues 252 to 302)
CC was identified using the "long probe" strategy used previously for TGF-
CC alpha. Long oligonucleotides (T1572-23) designed on the basis of the
CC partial protein sequence were used as hybridisation probes for the exon
CC in a human genomic DNA library. The TGF beta 1 exon was then used as a
CC probe for the isolation of TGF beta 1 cDNA (see AAT15270). DNA encoding
CC TGF beta 1 is useful for the recombinant production of the protein, which
CC is useful in, e.g. wound healing. (Updated on 25-MAR-2003 to correct PF
CC field.)
SQ Sequence_50 AA;

Query March 100.0%; Score 96; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps

QY      1 HANFCLGPCPYMSL 15
        |||||
Db       31 HANFCLGPCPYMSL 45

RESULT 6
AAR04075
ID AAR04075 standard; protein; 51 AA.
XX
AC AAR04075;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 31-MAY-1989 (first entry)
XX
DE Sequence of genomic fragment encoding a TGF-beta 1 exon.
XX
KW Transforming growth factor beta-3 (TGF beta 3); tumour cells;
KM growth inhibition.
XX
OS Homo sapiens.
XX
PN WC08912101-A.
XX
PD 14-DEC-1989.
XX
PF 08-JUN-1988; 88WO-US001945.
XX
PR 08-JUN-1988; 88WO-US001945.
XX
PA (GETH ) GENENTECH INC.
PT Derynck RMA, Goeddel DV;
PI
XX
DR WPI; 1990-007474/01.
DR P-PSDB; AAR04075.
XX
XX
PT Nucleotide sequence encoding transforming growth factor beta-3 - used as
PT a probe, or to produce Ygf beta-3, for growth inhibition of certain
XX normal and neoplastic cells, e.g. A549.
XX
PS Disclosure; Fig 2; 61pp; English.
CC This sequence encodes an exon of transforming growth factor-beta 1 (TGF-
beta 1) polypeptide corresponding to AA's 288-338 of mature TGF-beta 1.
```

CC The nucleic acid sequence encoding the second subtype of TGF-beta (TGF-beta 3) is useful as a probe or to produce TGF-beta 3 for both normal and CC neoplastic cell growth inhibition. (Updated on 31-OCT-2002 to add missing CC OS field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.)

CC Sequence 51 AA;

Query Match 100.0%; Score 96; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGPCPYIWSL 15
Db 31 HANFCLGPCPYIWSL 45

RESULT 7
AAW78788
ID AAW78788 standard; protein; 51 AA.

XX AAW78788;

XX 25-MAR-2003 (revised)
DT 21-DEC-1998 (first entry)

XX Human transforming growth factor-beta fragment (aa288-338).

XX Transforming growth factor-beta 1; TGF-beta 1; human.

XX Homo sapiens.

XX US5801231-A.

XX 01-SEP-1998.

XX 30-MAY-1995; 95US-00454468.

XX 22-MAR-1985; 85US-00715142.

XX 13-MAR-1987; 87US-00025423.

XX 04-AUG-1989; 89US-00389929.

XX 04-MAR-1992; 92US-00845893.

XX 05-NOV-1993; 93US-00147364.

XX (GERTH) GENENTECH INC.

XX Derynck RMA, Goeddel DV;

XX WPI; 1998-494840/42.

XX N-PSDB; AAV52936.

XX DNA encoding transforming growth factor-beta precursor sequence - useful for analysis to perform manipulations to increase yield of recombinant production of the protein.

XX Example 2; Fig 2; 26pp; English.

XX This polypeptide comprises amino acid residues 288-338 of human transforming growth factor-beta 1 precursor (preTGF-beta 1, see also CC AAW78785). It is encoded by an isolated fragment (see AAV52936) of the TGF-beta 1 gene. The invention relates to the recombinant production of CC TGF-beta. Nucleic acids encoding TGF-beta have been isolated and cloned into vectors which are replicated in bacteria and expressed in eukaryotic CC cells. TGF-beta recovered from transformed cells is used in known CC therapeutic applications. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 51 AA;

Query Match 100.0%; Score 96; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGPCPYIWSL 15

Db 31 HANFCLGPCPYIWSL 45

RESULT 8
ABB43879
ID ABB43879 standard; peptide; 51 AA.

XX ABB43879;

XX 04-FEB-2002 (first entry)

XX Peptide #11385 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

XX Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000669.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.

XX Claim 27; SEQ ID NO 36514; 639pp + Sequence listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring CC human gene expression in a sample derived from human foetal liver. The CC single exon nucleic acid probes may be used for predicting, measuring and CC displaying gene expression in samples derived from human fetal liver. The CC present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form CC part of the printed specification, but was obtained in electronic format CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 51 AA;

Query Match 100.0%; Score 96; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGPCPYIWSL 15
Db 31 HANFCLGPCPYIWSL 45

RESULT 9
AAM37799

ID AAM37799 standard; protein; 51 AA.

XX AAM37799;

XX 17-OCT-2001 (first entry)

XX Peptide #11836 encoded by probe for measuring placental gene expression.

XX

KW Probe; microarray; human; placenta; antenatal diagnosis;
KM genetic disorder.
XX
OS Homo sapiens.
XX WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX
DR Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
PS Claim 27; SEQ ID NO 38068; 654bp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP;
CC see A11315-A157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
SQ Sequence 51 AA;

Query Match 100.0%; Score 96; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGPCPYIWSL 15
DB 31 HANFCLGPCPYIWSL 45

RESULT 10
AAM77605
ID AAM77605 standard; protein; 51 AA.
XX
AC AAM77605;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed protein SEQ ID NO: 37911.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000668.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX
DR Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
XX
PS Example 4; SEQ ID NO 37911; 658bp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is a
CC protein encoded by one of the probes of the invention
XX
SQ Sequence 51 AA;

Query Match 100.0%; Score 96; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGPCPYIWSL 15
DB 31 HANFCLGPCPYIWSL 45

RESULT 11
ABG46640
ID ABG46640 standard; peptide; 51 AA.
XX
AC ABG46640;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human peptide encoded by genome-derived single exon probe SEQ ID 36305.
XX
KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.
XX
OS Homo sapiens.
XX
PN WO200186003-A2.
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US000665.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples.
XX
XX Claim 27; SEQ ID NO 36305; 634bp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC; the novel set of probes which hybridize at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC collected from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of the
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridization of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray, assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridization to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene, a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Karagenen syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a peptide/protein encoded by a single exon probe of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 51 AA;
Query Match 100.0%; Score 96; DB 5; Length 51;
Best Local Similarity 100.0%; Pred. NO. 5.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HANFCLGPCPYIWSL 15
DB 31 HANFCLGPCPYIWSL 45
RESULT 12
AAB68685
ID AAB68685 standard; protein; 60 AA.
XX
XX AAB68685;
AC
XX
XX 03-MAY-2001 (first entry)
DT
XX
XX Human TGFbeta1 protein #1.
DE
XX
XX Human; transforming growth factor beta2; TGFbeta2; SILEX;
KW systemic evolution of ligands by exponential enrichment.
XX
XX Homo sapiens.
OS
XX
XX WO200109156-A1.
PN

XX
XX 08-FEB-2001.
PD
XX
XX 26-JUL-2000; 2000WO-US020397.
PF
XX
XX 29-JUL-1999; 99US-00363939.
PR
XX
XX (NEXS-) NEXSTAR PHARM INC.
PA
XX
XX Pagratis N, Lochrie M, Gold L;
PI
XX
XX WPI; 2001-218217/22.
DR
XX
XX
XX New RNA ligand to human transforming growth factor beta2, useful as
PT pharmaceuticals, diagnostics and as immuno histochemical reagents.
PS
XX
XX Disclosure; Page 71, 178pp; English.
XX
XX The present invention relates to non-naturally occurring, high-affinity
CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
CC oligonucleotide ligands were identified by the SILEX method (SILEX stands
CC for Systemic Evolution of Ligands by Exponential Enrichment). The
CC oligonucleotide ligands are useful in any process in which binding to
CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
CC diagnostics, imaging agents and immunohistochemical reagents
XX
XX
SQ Sequence 60 AA;
Query Match 100.0%; Score 96; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. NO. 6.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HANFCLGPCPYIWSL 15
DB 40 HANFCLGPCPYIWSL 54
RESULT 13
AAW30331
ID AAW30331 standard; peptide; 62 AA.
XX
XX AAW30331;
AC
XX
XX 11-FEB-1998 (first entry)
DT
XX
XX
DE
XX
XX Fragment of growth factor TGFbeta1.
XX
XX Neurturin; human; haematopoietic cell; neuronal cell; stem cell; NT gene;
KW neurodegenerative disease; peripheral neuropathy; nervous system tumour;
KW amyotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; ischaemic stroke; acute brain injury; haemophilia;
KW acute spinal cord injury; multiple sclerosis; eosinophilia; lymphopaenia;
KW monocytopenia; neutropenia; anaemia; thrombocytopenia; neuroblastoma;
KW antibody; obesity; therapy; transforming growth factor beta; TGFbeta1;
KW growth factor; hybrid protein.
XX
XX
XX Homo sapiens.
OS
XX
XX WO9708196-A1.
PN
XX
XX 06-MAR-1997.
PD
XX
XX 27-AUG-1996; 96WO-US014065.
PF
XX
XX 28-AUG-1995; 95US-00519777.
PR
XX
XX (UNIW) UNIV WASHINGTON.
PA
XX
XX Johnson EM, Milbrandt JD, Kotzbauer PT, Lampe PA;
PI
XX
XX WPI; 1997-179176/16.
DR
XX
XX A novel growth factor Neurturin - used to treat neuro-degenerative and
PT

PT haematopoietic cell degeneration diseases, e.g. Alzheimer's disease and
 XT eosinopenia.
 PS Claim 93; Fig 17; 206pp; English.
 XX
 CC AAW30331-M30353 represent human growth factor fragments that are used in
 CC a hybrid polypeptide of the invention. These sequences form a hybrid with
 CC the human neuturin (NT) fragment shown in AAW30378. NT promotes the
 CC growth and differentiation of haematopoietic and neuronal cells, and
 CC their stem cells. The NT gene and protein are used to prevent or treat
 CC neurodegenerative diseases e.g. peripheral neuropathy, amyotrophic
 CC lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's
 CC disease, ischaemic stroke, acute brain injury, acute spinal cord injury,
 CC nervous system tumours, multiple sclerosis and infection; and
 CC haematopoietic cell degenerative diseases, e.g. eosinopenia, basopenia,
 CC lymphopenia, monocytopenia, neutropenia, anemia, thrombocytopenia,
 CC and stem cell insufficiencies. The NT protein and gene are also useful to
 CC treat neuroblastomas. Antibodies against NT and oligonucleotides (used as
 CC either probes or primers, corresponding to an exon of pre-pro-NT gene or
 CC flanking a target sequence) can be used for detecting NT in a sample or
 CC detecting mutations in the NT gene. Antisense sequences of the NT gene
 CC are used to treat diseases promoted by NT expression e.g. obesity
 CC
 XX Sequence 62 AA;
 SQ
 Query Match 100.0%; Score 96; DB 2; Length 62;
 Best Local Similarity 100.0%; Pred. No. 6.9e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HANFCLGCPYIWSL 15
 |||||
 Db 26 HANFCLGCPYIWSL 40
 |||||
 RESULT 14
 AAR22135
 ID AAR22135 standard; peptide; 65 AA.
 XX
 AC AAR22135;
 XX
 DT 25-MAR-2003 (revised)
 DT 10-JUL-1992 (first entry)
 XX
 DE PDGI subunit b.
 XX
 KM Platelet derived growth inhibitor alpha; TGF-beta; trypsin; pepsin;
 KM cell proliferation; eczema; immunosuppressant.
 XX
 OS Homo sapiens.
 XX
 PN EP475719-A.
 XX
 PD 18-MAR-1992.
 XX
 PF 10-SEP-1991; 91EP-00308239.
 XX
 PR 11-SEP-1990; 90JP-00238944.
 XX
 PA (NAKA/) NAKAMURA T.
 PA Nakamura T, Nakamura T;
 PI WPI; 1992-090304/12.
 DR WPI; 1992-090304/12.
 XX
 PT New platelet-derived growth regulating peptide-alpha - used for treatment
 PT of eczema, stimulation of bone growth and as immunosuppressant.
 XX
 PS Claim 2; Page 11; 21pp; English.
 XX
 CC The peptide is subunit b of PDGI alpha. It can be obtd. by treating
 CC transforming growth factor (TGF) beta with chymotrypsin or pepsin, or can
 CC be isolated from human blood platelets or by recombinant expression of
 CC DNA obtd. using RNA extd. from blood plasma. PDGI alpha is comprised of

CC subunits a, b and c bonded b-a-c. PDGI alpha can be used for controlling
 CC cell proliferation without the cancerous activity (transformation
 CC activity) associated with TGF-beta. PGFI- alpha can be used for
 CC activation and acceleration of the proliferation of epithelium cells in
 CC treating eczema, for stimulating osseous growth for bone formation or as
 CC an immuno- suppressant for immune diseases. See also AAR22134-6. (Updated
 CC on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 65 AA;
 Query Match 100.0%; Score 96; DB 2; Length 65;
 Best Local Similarity 100.0%; Pred. No. 7.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HANFCLGCPYIWSL 15
 |||||
 Db 40 HANFCLGCPYIWSL 54
 |||||
 RESULT 15
 AAY16697
 ID AAY16697 standard; peptide; 98 AA.
 XX
 AC AAY16697;
 XX
 DT 17-AUG-1999 (first entry)
 DT
 DE WO9914235 Seq ID No: 150.
 XX
 KM Growth factor; GF; persephin; neuron growth; cellular degeneration;
 KM peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke;
 KM Alzheimer's disease; Parkinson's disease; Huntington's disease; trauma;
 KM brain injury; spinal cord injury; nervous system tumour; infection;
 KM multiple sclerosis; cardiac muscle degeneration; injury; neurotoxins;
 KM metabolic disease; diabetes; renal dysfunction; neuturin.
 XX
 OS Unidentified.
 XX
 PN WO9914235-A1.
 XX
 PD 25-MAR-1999.
 XX
 PF 15-SEP-1998; 98WO-US019163.
 XX
 PR 16-SEP-1997; 97US-00931858.
 XX
 PA (UNIW) UNIV WASHINGTON.
 PA Johnson EM, Milbrandt JD, Kotzbauer PT, Lampe PA, Klein R;
 PI Desauvage F;
 PI WPI; 1999-244023/20.
 DR WPI; 1999-244023/20.
 XX
 PT New isolated persephin growth factor nucleic acids used to, e.g. promote
 PT neuronal growth.
 XX
 PS Disclosure; Page 175-176; 222pp; English.
 XX
 CC The invention relates to a novel isolated and purified growth factor (GF)
 CC that comprises persephin or a fragment or a conservatively substituted
 CC variant. The persephin GF polypeptides can promote the survival and
 CC growth of neurons and non-neuronal cells. The persephin GF polypeptides
 CC or polynucleotides can be used for preventing or treating cellular
 CC degeneration or insufficiency, e.g. neuronal degeneration resulting from
 CC peripheral neuropathy, amyotrophic lateral sclerosis, Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease, ischemic stroke,
 CC acute brain injury, acute spinal cord injury, nervous system tumours,
 CC multiple sclerosis, or infection, haematopoietic cell degeneration or
 CC insufficiency resulting from eosinopenia, anemia, thrombocytopenia, or
 CC stem-cell insufficiencies, cardiac muscle degeneration or insufficiency
 CC resulting from cardiomyopathy or congestive heart failure. They can also
 CC be used for treating e.g. peripheral nerve trauma or injury, exposure to
 CC neurotoxins, metabolic diseases such as diabetes or renal dysfunctions

CC and damage caused by infectious agents. The GF can also be used for
CC promoting the growth and/or differentiation of a cell in a culture
CC medium. The antisense polynucleotides can be used for treating a disease
CC condition mediated by expression of perlepin by a population of cells.
CC The products can also be used for detection and diagnosis
XX

SQ Sequence 98 AA;

Query Match 100.0%; Score 96; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGPPYIWSL 15
|||
Db 26 HANFCLGPPYIWSL 40

Search completed: June 14, 2005, 15:46:23
Job time : 88.9615 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2005, 15:34:23 ; Search time 80.1923 Seconds
(without alignments)
95.785 Million cell updates/sec

Title: US-09-831-253F-1
Perfect score: 96
Sequence: 1 HANFLGCPFYWSL 15

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	96	100.0	50 2 Q28240	Q28240 cervus elap
2	96	100.0	51 2 Q72487	Q72487 homo sapien
3	96	100.0	78 2 Q70316	Q70316 sus scrofa
4	96	100.0	101 2 Q9R184	Q9R184 meriones un
5	96	100.0	112 2 O02730	O02730 oryctolagus
6	96	100.0	124 2 Q95N80	Q95N80 canis famli
7	96	100.0	130 2 Q08714	Q08714 mesocricetu
8	96	100.0	315 1 TGF1_BOVIN	P18341 bos taurus
9	96	100.0	368 2 Q8R4D9	Q8R4D9 sigmodon hi
10	96	100.0	390 1 TGF1_CANFA	P54831 canis famli
11	96	100.0	390 1 TGF1_CAVPO	Q941Y6 cavia porce
12	96	100.0	390 1 TGF1_CERAE	P09533 cercopithec
13	96	100.0	390 1 TGF1_HORSE	O19011 equus caball
14	96	100.0	390 1 TGF1_HUMAN	P01137 homo sapien
15	96	100.0	390 1 TGF1_MOUSE	P04202 mus musculu
16	96	100.0	390 1 TGF1_PIG	P07200 sus scrofa
17	96	100.0	390 1 TGF1_RAT	P17246 rattus norv
18	96	100.0	390 1 TGF1_SHEEP	P50414 ovis aries
19	96	100.0	390 2 Q9TUM8	Q9TUM8 equus caball
20	82	85.4	373 1 TGF1_CHICK	P09531 gallus gall
21	77	80.2	412 1 TGF2_CHICK	P30371 gallus gall
22	74	77.1	382 1 TGF1_XENLA	P16176 xenopus lae
23	70	72.9	77 2 Q90YF8	Q90YF8 oncorhynch
24	70	72.9	86 2 Q28241	Q28241 cervus elap
25	70	72.9	88 2 Q90YF7	Q90YF7 oncorhynch
26	70	72.9	91 2 Q9MYZ1	Q9MYZ1 capra hircu
27	70	72.9	112 1 TGF2_BOVIN	P21214 bos taurus
28	70	72.9	224 2 Q8CDZ9	Q8CDZ9 mus musculu
29	70	72.9	255 2 Q921T1	Q921T1 mus musculu
30	70	72.9	361 2 Q98854	Q98854 cypripus ca
31	70	72.9	399 2 Q9ERB7	Q9ERB7 mesocricetu

32	70	72.9	410 2 Q66123	Q66123 brachydanio
33	70	72.9	410 2 Q7SZV3	Q7SZV3 brachydanio
34	70	72.9	411 2 Q7SZV4	Q7SZV4 brachydanio
35	70	72.9	413 1 TGF2_XENLA	P17247 xenopus lae
36	70	72.9	414 1 TGF2_CERAE	P61811 cercopithec
37	70	72.9	414 1 TGF2_HUMAN	P61812 homo sapien
38	70	72.9	414 1 TGF2_MOUSE	P27090 mus musculu
39	70	72.9	414 2 Q91VP5	Q91VP5 mus musculu
40	70	72.9	435 1 TGF2_PIG	P09858 sus scrofa
41	70	72.9	442 1 TGF2_RAT	Q07257 rattus norv
42	70	72.9	442 2 Q6T7C3	Q6T7C3 oryctolagus
43	69	71.9	62 2 Q90YF4	Q90YF4 pleuronecte
44	68	70.8	62 2 Q90ZJ7	Q90ZJ7 anguilla an
45	68	70.8	62 2 Q9DEP5	Q9DEP5 scophthalmu

ALIGNMENTS

RESULT 1
Q28240 PRELIMINARY; PRT; 50 AA.
AC Q28240;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Transforming growth factor beta 1 (TGF-beta 1) (Transforming growth factor B1) (Fragment).
GN Name=TGFBI; Synonyms=TGF beta-1, TGF-B1;
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervinae; Cervus.
OX NCBI_TaxId=9660;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Antler;
RX MEDLINE=98233260; PubMed=9571767;
RA DOI=10.1002/(SICI)1097-010X(19980501)281:1-36::AID-JB26>3.0.CO;2-D;
RA Francis S.M., Suttie J.M.;
RT "Detection of growth factors and proto-oncogene mRNA in the growing tip of red deer (Cervus elaphus) antler using reverse-transcriptase RT polymerase chain reaction (RT-PCR).";
RL J. Exp. Zool. 281:36-42(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Wagener A., Bliotner S., Pickel J.;
RT "Detection of growth factors in the testes of roe deer (Capreolus capreolus).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DERIVATIVES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -!- SUBUNIT: Homodimer; disulfide-linked (by similarity).
CC -!- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; U62110; AB05256.1; -.
DR EMBL; AF152591; AAF73230.1; -.
DR HSRP; P01137; IKLA.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR GO; GO:0008283; F: cell proliferation; IEA.
DR GO; GO:0000074; P: regulation of cell cycle; IEA.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF beta; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SMO0204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Glycoprotein; Growth factor; Mitogen.
FT NON_TER 1
FT CHAIN 1
FT <1 >50 TRANSFORMING GROWTH FACTOR BETA 1.

[illegible]

```

DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPRO01839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Growth factor.
FT NON TER 1 1 transforming growth factor beta 1.
FT CHAIN <1 >78
FT NON TER 78 78
SQ SEQUENCE 78 AA; 8981 MW; 1BA179EL47738152 CRC64;

Query Match 100.0%; Score 96; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGPCPYIMSL 15
Db 24 HANFCLGPCPYIMSL 38

RESULT 4
Q9R184 PRELIMINARY; PRT; 101 AA.
Q9R184
AC Q9R184;
DT 01-MAY-2000 (TRENMBLrel. 13, Created)
DT 01-MAY-2000 (TRENMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TRENMBLrel. 26, Last annotation update)
DE Transforming growth factor beta 1 (TGF-beta 1) (Fragment).
GN Name=TGFb1; Synonyms=TGF-BETA;
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH NODE;
RA Rao U.R., Klei T.R.;
RT "cDNA cloning of gerbil transforming growth factor-beta by PCR.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
CC THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
CC REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
CC DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF161218; AA045726.1; -.
DR HSSP; P01137; IKA.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR GO; GO:0008283; P: cell proliferation; IEA.
DR GO; GO:0000074; P: regulation of cell cycle; IEA.
DR InterPro; IPRO01839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR KW Glycoprotein; Growth Factor; Mitogen.
FT NON TER 1 1
FT CHAIN <1 >101 TRANSFORMING GROWTH FACTOR BETA 1.
FT DISULFID 1 10 BY SIMILARITY.
FT DISULFID 9 72 BY SIMILARITY.
FT DISULFID 71 71 INTERCHAIN (BY SIMILARITY).
FT NON TER 101 101
SQ SEQUENCE 101 AA; 11724 MW; ABF1CDA264AEFD CRC64;

Query Match 100.0%; Score 96; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 4.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGPCPYIMSL 15

```

Db 34 HANFCLGCPYIWSL 48

RESULT 5

002730 PRELIMINARY; PRT; 112 AA.
 002730; 097501;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Transforming growth factor beta 1 (TGF-beta 1) (Fragment).
 GN Name=TGFBI; Synonyms=TGF-beta-1;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Taylor T.K., James E.R., McGonigle S., Yoho E.R.;
 RL Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 2-99 FROM N.A.
 RA Inoue K., Kawabe Y., Kodama T.;
 RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
 CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
 CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
 CC THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
 CC REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
 CC DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 DR EMBL; AF000133; AAB53806.1; -.
 DR EMBL; AB020217; BAA36950.1; -.
 DR HSSP; P01137; 1KLA.
 DR GO; GO:0008083; F:growth factor activity; IEA.
 DR GO; GO:0008283; P:cell proliferation; IEA.
 DR GO; GO:000074; P:regulation of cell cycle; IEA.
 DR InterPro; IPR002400; GF_cyknob.
 DR InterPro; IPR001839; TGFb.
 DR Pfam; PF00019; TGF_beta.1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR ProDom; PD000357; TGFb.1.
 DR SMART; SM00204; TGFb.1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Glycoprotein; Growth factor; Mitogen.
 FT CHAIN 1
 FT NON_TER 1
 FT DISULFID 1 112 TRANSFORMING GROWTH FACTOR BETA 1.
 FT DISULFID 7 16 BY SIMILARITY.
 FT DISULFID 15 78 BY SIMILARITY.
 FT DISULFID 44 109 BY SIMILARITY.
 FT DISULFID 48 111 BY SIMILARITY.
 FT DISULFID 77 77 INTERCHAIN (BY SIMILARITY).
 FT CONFLICT 2 3 LD -> FS (IN REF. 2).
 FT CONFLICT 85 92 PLPTIYV -> ATMRVTTL (IN REF. 2).
 SQ SEQUENCE 112 AA; 12795 MW; 53CSBYD46355A6F3 CRC64;

Query Match 100.0%; Score 96; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 4,7e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 40 HANFCLGCPYIWSL 54

RESULT 6
 095N80 PRELIMINARY; PRT; 124 AA.
 AC 095N80;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Transforming growth factor beta 1 (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fontana S., Groene A., Baumgaertner W.;
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 DR EMBL; AF349538; AAK54072.1; -.
 DR HSSP; P01137; 1KLA.
 DR GO; GO:0008083; F:growth factor activity; IEA.
 DR InterPro; IPR001839; TGFb.
 DR Pfam; PF00019; TGF_beta.1.
 DR ProDom; PD000357; TGFb.1.
 DR SMART; SM00204; TGFb.1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Growth factor.
 FT NON_TER 1
 FT NON_TER 124
 SQ SEQUENCE 124 AA; 14329 MW; 21D185218E5556DB CRC64;

Query Match 100.0%; Score 96; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 5.1e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGCPYIWSL 15
 Db 55 HANFCLGCPYIWSL 69

RESULT 7
 008714 PRELIMINARY; PRT; 130 AA.
 AC 008714; 070331;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Transforming growth factor beta 1 (TGF-beta 1) (Fragment).
 GN Name=TGFBI;
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LG (SYR);
 RX MEDLINE=93304479; PubMed=8317544;
 RA Wong D.T., Donoff R.B., Yang J., Song B.Z., Matossian K., Nagura N.,
 RA Elvovic A., McBride J., Gallagher G., Todd R.;
 RT "Sequential expression of transforming growth factors alpha and beta 1
 RT by eosinophils during cutaneous wound healing in the hamster.";
 RL Am. J. Pathol. 143:130-142(1993).
 RN [2]
 RP SEQUENCE OF 26-115 FROM N.A.
 RC STRAIN=SYRIAN; TISSUE=SPLEEN;
 RX MEDLINE=98234044; PubMed=9573100;
 RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
 RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
 RT analysis of cytokine mRNA expression in experimental visceral
 RT leishmaniasis.";
 RL Infect. Immun. 66:2135-2142(1998).
 CC -1- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
 CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
 CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
 CC THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
 CC REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
 CC DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
 CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.

```

DR EMBL; X60296; CAA42838.1; -.
DR EMBL; AF046214; AAC40099.1; -.
DR PIR; I48196; I48196.
DR HSSP; P01137; IKLA.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR GO; GO:0008283; P: cell proliferation; IEA.
DR GO; GO:0000074; P: regulation of cell cycle; IEA.
DR InterPro; IPR01839; TGFb.
DR Pfam; PF00019; TGF beta; 1.
DR Prodom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Glycoprotein; Growth Factor; Mitogen.
FT PROPEP <1 18 TRANSFORMING GROWTH FACTOR BETA 1.
FT CHAIN 19 130 BY SIMILARITY.
FT DISULFID 25 34 BY SIMILARITY.
FT DISULFID 33 96 BY SIMILARITY.
FT DISULFID 66 129 BY SIMILARITY.
FT DISULFID 95 95 INTERCHAIN (BY SIMILARITY).
FT CONFLICT 93 93 G -> S (IN REF. 2).
SQ SEQUENCE 130 AA; 14997 MW; 8B41DD6CF39CA77 CRC64;

Query Match 100.0%; Score 96; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGPCPYTWSL 15
DB 58 HANFCLGPCPYTWSL 72

RESULT 8
TGFI_BOVIN STANDARD; PRT; 315 AA.
ID TGFI_BOVIN
AC P18341;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1) (Fragment).
GN Name=TGFb1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91042552; PubMed=3153459;
RA van Obberghen-Schilling E., Kondalah P., Ludwig R.L., Sporn M.B.,
RA Baker C.C.;
RT "Complementary deoxyribonucleic acid cloning of bovine transforming
RT growth factor-beta 1."
RL Mcl. Endocrinol. 1:693-698 (1987).
RN [2]
RP SUBUNITS.
RC TISSUE=Bone;
RX MEDLINE=92129307; PubMed=1733936;
RA Ogawa Y., Schmidt D.K., Daech J.R., Chang R.J., Glaser C.B.;
RT "Purification and characterization of transforming growth factor-beta
RT 2,3 and -beta 1,2 heterodimers from bovine bone."
RL J. Biol. Chem. 267:2325-2328 (1992).
DE -1- FUNCTION: TGF-beta is a multifunctional peptide that control
CC proliferation, differentiation, and other functions in many cell
CC types. Many cells synthesize TGF-beta and essentially all of them
CC have specific receptors for this peptide. TGF-beta regulates the
CC actions of many other peptide growth factors and determines a
CC positive or negative direction of their effects. Play an important
CC role in bone remodelling. It is a potent stimulator of
CC osteoblastic bone formation, causing chemotaxis, proliferation and
CC differentiation in committed osteoblasts (by similarity).
CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
CC covalently linked to a latency-associated peptide (LAP) homodimer.

```

```

CC The inactive complex can contain a latent TGF-beta binding protein
CC (by similarity). The active form is a homodimer of mature TGF-beta
CC 1; disulfide-linked. Heterodimers of TGF-beta 1/2 have been found
CC in bone.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1
CC and LAP (by similarity).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M36271; AAA30778.1; -.
DR PIR; A40057; A40057.
DR HSSP; P01137; IKLA.
DR InterPro; IPR002400; GF_Cybknot.
DR InterPro; IPR003911; TGF_TGFb.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR01423; TGFbBETA.
DR Prodom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Glycoprotein; Growth Factor; Mitogen.
FT NON_TER 1 1
FT PROPEP <1 203
FT CHAIN 204 315 Transforming growth factor beta 1.
FT DISULFID 210 219 By similarity.
FT DISULFID 218 281 By similarity.
FT DISULFID 247 312 By similarity.
FT DISULFID 251 314 By similarity.
FT DISULFID 280 280 Interchain (By similarity).
FT CARBOHYD 7 7 N-linked (GlcNAc...) (By similarity).
FT CARBOHYD 61 61 N-linked (GlcNAc...) (By similarity).
FT CARBOHYD 101 101 N-linked (GlcNAc...) (By similarity).
FT SITE 169 171 Cell attachment site (Potential).
SQ SEQUENCE 315 AA; 36269 MW; C2717A23D994E008 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGPCPYTWSL 15
DB 243 HANFCLGPCPYTWSL 257

RESULT 9
ID Q8R4D9 PRELIMINARY; PRT; 368 AA.
AC Q8R4D9;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Transforming growth factor beta-1 protein (Fragment).
GN Name=Tgfb1;
OS Sismodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
OC NCBI_Taxid=42415;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14980081; DOI=10.1089/107999004772719873;
RA Blanco J.C., Pletneva L., Boukhalova M., Richardson J.Y.,

```

RA Harris K.A., Prince G.A.;
 RT "The cotton rat: an underutilized animal model for human infectious
 RT diseases can now be exploited using specific reagents to cytokines,
 RT chemokines, and interferons";
 RL J. Interleukin Cytochrome Res. 24:21-28(2004).
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 DR EMBL; AF480858; AAL87199.1; -.
 DR HSSP; P01137; IKLA.
 DR GO; GO:0008063; F:transforming growth factor beta receptor bi. . .; IEA.
 DR GO; GO:0005160; F:transforming growth factor beta receptor bi. . .; IEA.
 DR GO; GO:0016049; P:cell growth; IEA.
 DR InterPro; IPR002400; GF_cybknot.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR003939; TGFb.N.
 DR InterPro; IPR001111; TGFb.N.
 DR InterPro; IPR003911; TGF_TGFb.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR Pfam; PF00019; TGF_beta; 1.
 DR PRINTS; PRO0438; GFCYSKNOT.
 DR PRINTS; PRO1423; TGFbeta.
 DR PRINTS; PRO1424; TGFbeta1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Growth factor.
 FT NON TER
 SQ SEQUENCE 368 AA; 41905 MW; A5C91207B0468B4A CRC64;
 Query Match 100.0%; Score 96; DB 2; Length 368;
 Best Local Similarity 100.0%; Pred. No. 1,3e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWSL 15
 Db 296 HANFCLGCPYIWSL 310

RESULT 10
 TGFI_CANPA STANDARD; PRT; 390 AA.
 AC P54831;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).
 GN Name=TGFb1;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Jugular vein endothelial;
 RX MEDLINE=95237630; PubMed=7721110; DOI=10.1016/0378-1119(94)00903-6;
 RA Manning A.M., Auchampach J.A., Drong R.F., Slichtom J.L.;
 RT "Cloning of a canine cDNA homologous to the human transforming growth
 RT factor-beta 1-encoding gene";
 RL Gene 155:307-308(1995).
 CC -1- FUNCTION: TGF-beta is a multifunctional peptide that control
 CC proliferation, differentiation, and other functions in many cell
 CC types. Many cells synthesize TGF-beta and essentially all of them
 CC have specific receptors for this peptide. TGF-beta regulates the
 CC actions of many other peptide growth factors and determines a
 CC positive or negative direction of their effects. Play an important
 CC role in bone remodeling. It is a potent stimulator of
 CC osteoblastic bone formation, causing chemotaxis, proliferation and
 CC differentiation in committed osteoblasts (By similarity).
 CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
 CC covalently linked to a latency-associated peptide (LAP) homodimer.
 CC The inactive complex can contain a latent TGF-beta binding
 CC protein. The active form is a homodimer of mature TGF-beta 1;
 CC disulfide-linked (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1
 CC and LAP (By similarity).
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb.ch/announce/>
 CC or send an email to license@isb.sib.ch).
 CC -----
 DR EMBL; I34956; AAA51458.1; -.
 DR PIR; JC4023; JC4023.
 DR HSSP; P01137; IKLA.
 DR InterPro; IPR002400; GF_cybknot.
 DR InterPro; IPR003911; TGF_TGFb.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb.N.
 DR Pfam; PF00019; TGF_beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PRO0438; GFCYSKNOT.
 DR PRINTS; PRO1423; TGFbeta.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Glycoprotein; Growth factor; Mitogen; Signal.
 FT SIGNAL
 FT PROPEP 1 29
 FT CHAIN 30 278
 FT FT CHAIN 279 390
 FT FT DISULFID 285 294
 FT FT DISULFID 293 356
 FT FT DISULFID 322 387
 FT FT DISULFID 326 389
 FT FT DISULFID 355 355
 FT FT CARBOHYD 82 85
 FT FT CARBOHYD 136 136
 FT FT CARBOHYD 176 176
 FT SITE 244 246
 SQ SEQUENCE 390 AA; 44185 MW; EB4780EB8B7B590E CRC64;
 Query Match 100.0%; Score 96; DB 1; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1,4e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWSL 15
 Db 318 HANFCLGCPYIWSL 332

RESULT 11
 TGFI_CANPA STANDARD; PRT; 390 AA.
 AC Q921Y6; Q902H3; Q9R148;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).
 GN Name=TGFb1;
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Hartley;
 RA Teevan A., McMurray D.N., Yoshimura T.;
 RT "Guinea pig transforming growth factor-beta in peritoneal exudates
 RT after BCG vaccination";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 265-382 FROM N.A.

RX MEDLINE=99144670; PubMed=10025978; DOI=10.1016/S1043-4666(98)90002-3;
 RA Scarozza A.M., Ramasingh A.I., Wicher V., Wicher K.;
 RT "spontaneous cytokine gene expression in normal guinea pig blood and
 RL tissues";
 RT Cytokine 10:851-859(1998).
 RN [3]
 RC SEQUENCE OF 279-371 FROM N.A.
 RP STRAIN=Hartley; TISSUE=Trachea;
 RA Morishima Y., Uchida Y., Nomura A., Ishii Y., Sakamoto T.,
 RA Sekizawa K.;
 RT "Guinea-pig transforming growth factor-beta expression in injured
 RT tracheal epithelium";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Multifunctional peptide that controls proliferation,
 CC differentiation, and other functions in many cell types. Many
 CC cells synthesize TGF-beta 1 and essentially all of them have
 CC specific receptors for this peptide. TGF-beta 1 regulates the
 CC actions of many other peptide growth factors and determines a
 CC positive or negative direction of their effects. Play an important
 CC role in bone remodelling. It is a potent stimulator of
 CC osteoblastic bone formation, causing chemotaxis, proliferation and
 CC differentiation in committed osteoblasts (By similarity).
 CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
 CC covalently linked to a latency-associated peptide (LAP) homodimer.
 CC The inactive complex can contain a latent TGF-beta binding
 CC protein. The active form is a homodimer of mature TGF-beta 1;
 CC disulfide-linked (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PMW: Glycosylated. The precursor is cleaved into mature TGF-beta 1
 CC and LAP (By similarity).
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>
 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL; AF191297; AAF02760.1; -;
 DR EMBL; AF097509; AAC83807.1; -;
 DR EMBL; AF169347; AAD49347.1; -;
 DR HSSP; P01137; 1KLA.
 DR InterPro; IPR002400; GF_cyknoc.
 DR InterPro; IPR003911; TGF_TGFB.
 DR InterPro; IPR001839; TGFB_N.
 DR InterPro; IPR001111; TGFB_N.
 DR Pfam; PF00688; TGFB_beta_1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PRINTS; PR01423; TGBBETA.
 DR PRODOM; PD000357; TGFB_1.
 DR SMART; SM00204; TGFB_1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 DR Glycoprotein; Growth Factor; Mitogen; Signal.
 FT SIGNAL 1 29
 FT PROPEP 30 278
 FT CHAIN 279 390
 FT DISULFID 285 294
 FT DISULFID 293 356
 FT DISULFID 322 387
 FT DISULFID 326 389
 FT DISULFID 355 355
 FT CARBOHYD 82 82
 FT CARBOHYD 136 136
 FT CARBOHYD 176 176
 FT SIRE 244 246
 FT CONFLICT 279 279
 FT CONFLICT 286 286
 FT CONFLICT 309 309
 FT CONFLICT 322 322
 FT CONFLICT 322 322
 C -> R (in Ref. 2).

FT CONFLICT 350 350 A -> G (in Ref. 2).
 SQ SEQUENCE 390 AA; 44328 MW; 1539F849BA0C0FF1 CRC64;
 Query Match 100.0%; Score 96; DB 1; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1.4e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HANFCLGPCPYMSL 15
 DB 318 HANFCLGPCPYMSL 332
 RESULT 12
 TGF1 CERAE STANDARD; PRT; 390 AA.
 ID TGF1 CERAE
 AC P09533;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).
 GN Name=TGFBI;
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 CC Cercopithecinae; Cercopithecus.
 CC NCBI TaxID=9534;
 OX [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=87246074; PubMed=3474130;
 RA Sharples K., Plowman G.D., Rose T.M., Twardzik D.R., Purchio A.F.;
 RT "Cloning and sequence analysis of simian transforming growth factor-
 RT beta cDNA";
 RL J. Biol. Chem. 263:14211-14215 (1988).
 RN [3]
 RP CHARACTERIZATION.
 RP PubMed=3185545;
 RA Gentry L.E., Lioubin M.N., Purchio A.F., Marguardt H.;
 RT "Molecular events in the processing of recombinant type 1 pre-pro-
 RT transforming growth factor beta to the mature polypeptide";
 RL Mol. Cell. Biol. 8:4162-4168(1988).
 CC -1- FUNCTION: Multifunctional peptide that controls proliferation,
 CC differentiation, and other functions in many cell types. Many
 CC cells synthesize TGF-beta 1 and essentially all of them have
 CC specific receptors for this peptide. TGF-beta 1 regulates the
 CC actions of many other peptide growth factors and determines a
 CC positive or negative direction of their effects. Play an important
 CC role in bone remodelling. It is a potent stimulator of
 CC osteoblastic bone formation, causing chemotaxis, proliferation and
 CC differentiation in committed osteoblasts (By similarity).
 CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
 CC covalently linked to a latency-associated peptide (LAP) homodimer.
 CC The inactive complex can contain a latent TGF-beta binding
 CC protein. The active form is a homodimer of mature TGF-beta 1;
 CC disulfide-linked.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PMW: Glycosylated. The precursor is cleaved into mature TGF-beta 1
 CC and LAP, which remains non-covalently linked to mature TGF-beta 1
 CC rendering it inactive.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial

CC entries requires a license agreement (See <http://www.isb-sib.ch/announce>
or send an email to license@sib-sib.ch).

DR EMIL; M16658; AAA35369.1; .
DR PIR; A26960; A26960.
DR HSSP; P01137; 1KLA.
DR InterPro; IPR002400; GF_cyknct.
DR InterPro; IPR003911; TGF_TGFB.
DR InterPro; IPR001839; TGFB.
DR InterPro; IPR001111; TGFB_N.
DR Pfam; PF00019; TGF_beta_1.
DR Pfam; PF00688; TGFB_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNCT.
DR PRINTS; PR01433; TGBBETA.
DR ProDom; PD000357; TGFB; 1.
DR SMART; SMO0204; TGFB; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Glycoprotein; Growth_Factor; Mitogen; Signal.
FT SIGNAL 1 29
FT PROPEP 30 278 Latency-associated peptide.
FT CHAIN 279 390 Transforming growth factor beta 1.
FT DISULFID 285 294 By similarity.
FT DISULFID 293 356 By similarity.
FT DISULFID 322 387 By similarity.
FT DISULFID 326 389 By similarity.
FT DISULFID 355 355 By similarity.
FT CARBOHYD 82 82 N-linked (GlcNAc...)
FT CARBOHYD 136 136 N-linked (GlcNAc...)
FT CARBOHYD 176 176 N-linked (GlcNAc...)
FT SITE 244 246 Cell attachment site (Potential).
SQ SEQUENCE 390 AA; 44356 MW; DPF6352BAB44320E CRC64;

QY Query Match 100.0%; Score 96; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 1,4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

Dd 318 HANCLGPCPYINSL 332

RESULT 13

ID	TGFI_HORSE	STANDARD:	PRT:	390 AA.
AC	O19011;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DB	Transforming growth factor beta 1 precursor (TGF-beta 1).			
GN	Name=TGFB1;			
OS	Equus caballus (Horse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euteria; Perissodactyla; Equidae; Equus.			
OX	NCBI_TaxId=9796;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lymph node;			
RX	MEDLINE=98185507; PubMed=9524819;			
RA	"Penha-Goncalves M.N., Onions D.E., Nicolson L.;			
RT	"Cloning and sequencing of equine transforming growth factor-beta 1			
RL	(TGF beta-1) cDNA.";			
RT	DNA Seq. 7:375-378(1997).			
CC	-1- FUNCTION: TGF-beta is a multifunctional peptide that control			
CC	proliferation, differentiation, and other functions in many cell			
CC	types. Many cells synthesize TGF-beta and essentially all of them			
CC	have specific receptors for this peptide. TGF-beta regulates the			
CC	actions of many other peptide growth factors and determines			
CC	positive or negative direction of their effects. Play an important			
CC	role in bone remodelling. It is a potent stimulator of			
CC	osteoblastic bone formation, causing chemotaxis, proliferation and			
CC	differentiation in committed osteoblasts (by similarity).			
CC	SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-			
CC				

The inactive complex can contain a latent TGF-beta binding protein. The active form is a homodimer of mature TGF-beta 1; disulfide-linked (By similarity).

-1- SUBCELLULAR LOCATION: Secreted.

-1- Ptm: glycosylated. The precursor is cleaved into mature TGF-beta 1 and LAP (By similarity).

-1- SIMILARITY: Belongs to the TGF-beta family.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce> or send an email to license@isb-sib.ch).

CC EMBL; X99438; CAA67801.1; -. CC DR HSSP; P01137; KILA. CC DR InterPro; IPR002400; GF_cysknob. CC DR InterPro; IPR003911; TGF_TGFB. CC DR InterPro; IPR001839; TGFB. CC DR InterPro; IPR001111; TGFB_N. CC DR Pfam; PF00019; TGF_beta; 1. CC DR Pfam; PF00688; TGFB_propeptide; 1. CC DR PRINTS; PR00438; GRCYSKNOB. CC DR PRINTS; PR01423; TGPBETA. CC DR ProDom; PD000357; TGFB; 1. CC DR SMART; SM00204; TGFB; 1. CC DR PROSITE; PS00250; TGF_BETA_1; 1. CC KW Glycoprotein; Growth_Factor; Mitogen; Signal. CC FT SIGNAL 1 29 By similarity. CC FT PROPEP 30 278 Latency-associated peptide (By similarity). CC FT CHAIN 279 390 Transforming growth factor beta 1. CC FT DISULFID 285 294 By similarity. CC FT DISULFID 293 356 By similarity. CC FT DISULFID 322 387 By similarity. CC FT DISULFID 326 389 By similarity. CC FT DISULFID 355 355 Interchain (By similarity). CC FT CARBOHYD 82 82 N-linked (GLCNAC...) (By similarity). CC FT CARBOHYD 136 136 N-linked (GLCNAC...) (By similarity). CC FT CARBOXYD 176 176 N-linked (GLCNAC...) (By similarity). CC SQ SEQUENCE 390 AA; 43974 MW; A6BD15F44549691 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 1; Ae-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFGCPCEYIWSL 15
DB 318 HANFGCPCEYIWSL 332

RESULT 14
TGFI_HUMAN STANDARD; PRT; 390 AA.
AC P01137; O9UCG4; DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN Name=TFB1; Synonyms=TGFB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=87174845; PubMed=3470709;
RX Deynck R., Rhee L., Chen E.Y., van Tilburg A.;
RT "Intron-exon structure of the human transforming growth factor-beta
precursor gene."; NL Nucleic Acids Res. 15:3188-3189(1987).

[2]
 RA SEQUENCE FROM N.A., AND VARIANT PRO-10.
 RX MEDLINE=85296301; PubMed=3861940;
 RA Derynck R., Jarrett J.A., Chen E.Y., Eaton D.H., Bell J.R.,
 RA Asoian R.K., Roberts A.B., Sporn M.B., Goeddel D.V.,
 RT "Human transforming growth factor-beta complementary DNA sequence and
 RT expression in normal and transformed cells.";
 RL Nature 316:701-705(1985).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ductodenum, and Eye;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Holys S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalski J., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 279-390 FROM N.A.
 RC TISSUE=Carcinoma;
 RX Urushizaki Y., Niteu Y., Terui T., Koshida Y., Mahara K., Kohgo Y.,
 RA Urushizaki I., Takahashi Y., Ito H.,
 RT "Cloning and expression of the gene for human transforming growth
 RT factor-beta in Escherichia coli.";
 RL Tumor Res. 22:41-55(1987).
 RN [5]
 RP SEQUENCE OF 279-329.
 RC TISSUE=Bladder carcinoma;
 RX MEDLINE=93229900; PubMed=8471846; DOI=10.1006/prep.1993.1019;
 RA Bourdel L., Lin C.-H., Lauren S.L., Elmore R.H., Sugrman B.J.,
 RA Hu S., Westcott K.R.,
 RT "Recombinant human transforming growth factor-beta 1: expression by
 RT Chinese hamster ovary cells, isolation, and characterization.";
 RL Protein Expr. Purif. 4:130-140(1993).
 RN [6]
 RP SEQUENCE OF 279-301.
 RX MEDLINE=85131019; PubMed=2982829;
 RA Massague J., Li X.B.,
 RT "Cellular receptors for type beta transforming growth factor. Ligand
 RT binding and affinity labeling in human and rodent cell lines.";
 RL J. Biol. Chem. 260:2636-2645(1985).
 RN [7]
 RP SEQUENCE OF 30-42 AND 279-290, AND CHARACTERIZATION.
 RX PubMed=3162913;
 RA Miyazono K., Hellman U., Wernstedt C., Heldin C.H.,
 RT "Latent high molecular weight complex of transforming growth factor
 RT beta 1. Purification from human platelets and structural
 RT characterization.";
 RL J. Biol. Chem. 263:6407-6415(1988).
 RN [8]
 RP REVIEW.
 RX PubMed=9150447;
 RA Munger J.S., Harpel J.G., Gleizes P.E., Mazzieri R., Nunes I.,
 RA Rifkin D.B.,
 RT "Latent transforming growth factor-beta: structural features and
 RT mechanisms of activation.";
 RL Kidney Int. 51:1376-1382(1997).
 RN [9]
 RP
 RP STRUCTURE BY NMR OF 279-390.
 RX MEDLINE=93144319; PubMed=8424942;
 RA Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez K.A.,
 RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
 RA Torchia D.A.,
 RT "Transforming growth factor beta 1: NMR signal assignments of the
 RT recombinant protein expressed and isotopically enriched using Chinese
 RT hamster ovary cells.";
 RL Biochemistry 32:1152-1163(1993).
 RN [10]
 RP STRUCTURE BY NMR OF 279-390.
 RX MEDLINE=93144320; PubMed=8424943;
 RA Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez K.A.,
 RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
 RA Torchia D.A.,
 RT "Transforming growth factor beta 1: secondary structure as determined
 RT by heteronuclear magnetic resonance spectroscopy.";
 RL Biochemistry 32:1164-1171(1993).
 RN [11]
 RP STRUCTURE BY NMR OF 279-390.
 RX MEDLINE=96266150; PubMed=8679613; DOI=10.1021/b1960494g;
 RA Hick A.P., Archer S.J., Olan S.W., Roberts A.B., Sporn M.B.,
 RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
 RA Torchia D.A.,
 RT "Transforming growth factor beta 1: three-dimensional structure in
 RT solution and comparison with the X-ray structure of transforming
 RT growth factor beta 2.";
 RL Biochemistry 35:8517-8534(1996).
 RN [12]
 RP TISSUE SPECIFICITY.
 RX PubMed=11746498; DOI=10.1002/jcb.1249;
 RA Shur I., Lokiec F., Blalberg I., Benayahu D.,
 RT "Differential gene expression of cultured human osteoblasts.";
 RL J. Cell. Biochem. 83:547-553(2001).
 RN [13]
 RP VARIANT PRO-10.
 RX PubMed=9783545;
 RA Yamada Y., Myauchi A., Goto J., Takagi Y., Okuzumi H., Kanematsu M.,
 RA Hase M., Takai H., Harada A., Ikeda K.,
 RT "Association of a polymorphism of the transforming growth factor-beta1
 RT gene with genetic susceptibility to osteoporosis in postmenopausal
 RT Japanese women.";
 RL J. Bone Miner. Res. 13:1569-1576(1998).
 RN [14]
 RP VARIANTS CED CVS-218; HIS-218 AND ARG-225.
 RX PubMed=10973241; DOI=10.1038/79128;
 RA Kinoshita A., Saito T., Tomita H., Makita Y., Yoshida K., Ghadami M.,
 RA Yamada K., Kondo S., Ikegawa S., Nishimura G., Fukushima Y.,
 RA Nakagomi T., Saito H., Sugimoto T., Kamegaya M., Hise K., Murray J.C.,
 RA Taniguchi N., Nishikawa N., Yoshitake K.,
 RT "Domain-specific mutations in TGFBI result in Camurati-Engelmann
 RT disease.";
 RL Nat. Genet. 26:19-20(2000).
 RN [15]
 RP VARIANTS CED HIS-81; CVS-218 AND ARG-225.
 RX PubMed=11062463; DOI=10.1038/81563;
 RA Janssens K., Gershoni-Baruch R., Guanabens N., Mlgone N., Raleton S.,
 RA Bonduelle M., Lissens W., Van Maldergem L., Vanheesacker F.,
 RA Verbruggen L., Van Hul W.,
 RT "Mutations in the gene encoding the latency-associated peptide of TGF-
 RT beta 1 cause Camurati-Engelmann disease.";
 RL Nat. Genet. 26:273-275(2000).
 RN [16]
 RP VARIANT PRO-10.
 RX PubMed=12202987; DOI=10.1007/s100380200069;
 RA Watanabe Y., Kinoshita A., Yamada T., Ohta T., Kishino T.,
 RA Matsuno N., Ishikawa M., Nishikawa N., Yoshitake K.,
 RT "A catalog of 106 single-nucleotide polymorphisms (SNPs) and 11 other
 RT types of variations in genes for transforming growth factor-beta1
 RT (TGF-beta1) and its signaling pathway.";
 RL J. Hum. Genet. 47:478-483(2002).
 RN [17]
 RP CHARACTERIZATION OF VARIANTS CED HIS-81; CVS-218; ASP-222 AND ARG-225.
 RX PubMed=12202987; DOI=10.1007/s100380200069;
 RA Watanabe Y., Kinoshita A., Yamada T., Ohta T., Kishino T.,
 RA Matsuno N., Ishikawa M., Nishikawa N., Yoshitake K.,
 RT "A catalog of 106 single-nucleotide polymorphisms (SNPs) and 11 other
 RT types of variations in genes for transforming growth factor-beta1
 RT (TGF-beta1) and its signaling pathway.";
 RL J. Hum. Genet. 47:478-483(2002).
 RN [17]

CC PubMed=12493741; DOI=10.1074/jbc.M208857200;
RA Janssens K., ten Dijke P., Ralston S.H., Bergmann C., Van Hul W.;
RT "Transforming growth factor-beta-1 mutations in Camurati-Engelmann
RT disease lead to increased signaling by altering either activation or
RT secretion of the mutant protein";
RL J. Biol. Chem. 278:7718-7724(2003).
RN [18]
RP CHARACTERIZATION OF VARIANT CVS-218.
RA PubMed=12843182; DOI=10.1210/jc.2002-020564;
RC McGowan N.W., MacPherson H., Janssens K., Van Hul W., Frith J.C.,
RA Fraser W.D., Ralston S.H., Helfrich M.H.;
RT "A mutation affecting the latency-associated peptide of TGFbeta1 in
RT Camurati-Engelmann disease enhances osteoclast formation in vitro";
RL J. Clin. Endocrinol. Metab. 88:3321-3326(2003).
CC -1- FUNCTION: Multifunctional peptide that controls proliferation,
CC differentiation, and other functions in many cell types. Many
CC cells synthesize TGF-beta 1 and essentially all of them have
CC specific receptors for this peptide. TGF-beta 1 regulates the
CC actions of many other peptide growth factors and determines a
CC positive or negative direction of their effects. Play an important
CC role in bone remodeling. It is a potent stimulator of
CC osteoblastic bone formation, causing chemotaxis, proliferation and
CC differentiation in committed osteoblasts (by similarity).
CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
CC covalently linked to a latency-associated peptide (LAP) homodimer.
CC The inactive complex can contain a latent TGF-beta binding
CC protein. The active form is a homodimer of mature TGF-beta 1;
CC disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Highly expressed in bone.
CC -1- INDUCTION: Activated in vitro at pH below 3.5 and over 12.5.
CC -1- PTM: Glycosylated (By similarity). The precursor is cleaved into
CC mature TGF-beta 1 and LAP.
CC -1- POLYMORPHISM: In post-menopausal Japanese women, the frequency of
CC Leu-10 is higher in subjects with osteoporosis than in controls.
CC -1- DISEASE: Defects in TGFBI are the cause of Camurati-Engelmann

Query Match 100.0%; Score 96; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 1,4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGCPYIMSL 15
Db 318 HANFCLGCPYIMSL 332

RESULT 15
TGF1 MOUSE STANDARD; PRT; 390 AA.
ID TGF1 MOUSE
AC P04202;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN Name=Tgfb1;
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=86168129; PubMed=3007454;
RT Derynck R., Jarrett J.A., Chen E.Y., Goeddel D.V.;
RT "The murine transforming growth factor-beta precursor";
RL J. Biol. Chem. 261:4377-4379(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BAJB/c;
RA MEDLINE=96095545; PubMed=8522200; DOI=10.1016/0378-1119(95)00460-N;
RA Guron C., Sudarshan C., Raghow R.;
RT "Molecular organization of the gene encoding murine transforming
RT growth factor beta 1";
RL Gene 165:325-326(1995).

CC [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6, and NOD/Lt; TISSUE=Spleen;
RA Poliot L., Benoist C., Mathis D.;
RT "Transforming growth factor-beta 1 sequence and expression: no
RT difference between NOD/Lt and C57BL/6 mouse strains";
RN Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary gland;
RA MEDLINE=2238257; PubMed=1247932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Ditschenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein W.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: TGF-beta is a multifunctional peptide that control
CC proliferation, differentiation, and other functions in many cell
CC types. Many cells synthesize TGF-beta and essentially all of them
CC have specific receptors for this peptide. TGF-beta regulates the
CC actions of many other peptide growth factors and determines a
CC positive or negative direction of their effects. Play an important
CC role in bone remodeling. It is a potent stimulator of
CC osteoblastic bone formation, causing chemotaxis, proliferation and
CC differentiation in committed osteoblasts (by similarity).
CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
CC covalently linked to a latency-associated peptide (LAP) homodimer.
CC The inactive complex can contain a latent TGF-beta binding
CC protein. The active form is a homodimer of mature TGF-beta 1;
CC disulfide-linked (by similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1
CC and LAP (by similarity).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M13177; AAA40423.1; -;
DR EMBL; L42462; AAB00138.1; -;
DR EMBL; L42456; AAB00138.1; JOINED.
DR EMBL; L42457; AAB00138.1; JOINED.
DR EMBL; L42458; AAB00138.1; JOINED.
DR EMBL; L42459; AAB00138.1; JOINED.
DR EMBL; L42460; AAB00138.1; JOINED.
DR EMBL; L42461; AAB00138.1; JOINED.
DR EMBL; AJ009862; CAA08900.1; -;
DR EMBL; BC013738; AAH13738.1; -;
DR PIR; A01396; WPM52.
DR HSSP; P01137; IKA.
DR MGd; MG1:98725; Tgfb1.
DR GO; GO:0005578; C:extracellular matrix; IDA.
DR GO; GO:0006954; P:inflammatory response; IMP.

DR GO; GO:0007515; P:lymph gland development; IMP.
 DR GO; GO:0008220; P:necrosis; IMP.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
 DR GO; GO:0042127; P:regulation of cell proliferation; IDA.
 DR GO; GO:0016202; P:regulation of myogenesis; IDA.
 DR GO; GO:0042306; P:regulation of protein-nucleus import; IDA.
 DR GO; GO:0007179; P:transforming growth factor beta receptor si. . .; IDA.
 DR InterPro; IPR002400; GF cyknot.
 DR InterPro; IPR003911; TGF_TGFB.
 DR InterPro; IPR001839; TGF.
 DR InterPro; IPR011111; TGF_beta.
 DR Pfam; PF00019; TGF_beta; 1.
 DR PRINTS; PR00438; GFCSKNOT.
 DR PRINTS; PR01423; TGFbeta.
 DR ProDom; PD000357; TGFb; 1.
 DR PROSITE; PS00250; TGF_beta_1; 1.
 DR GlycoProtein; Growth factor; Mitogen; Signal.
 FT SIGNAL 1 29 By similarity.
 FT PROPEP 30 278 Latency-associated peptide.
 FT CHAIN 279 390 Transforming growth factor beta 1.
 FT DISULFID 285 294 By similarity.
 FT DISULFID 293 356 By similarity.
 FT DISULFID 322 387 By similarity.
 FT DISULFID 326 389 By similarity.
 FT DISULFID 355 355 Interchain (By similarity).
 FT CARBOHYD 82 82 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 136 136 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 176 176 N-linked (GlcNAc...) (By similarity).
 FT SITE 244 246 Cell attachment site (Potential).
 SQ SEQUENCE 390 AA; 44310 MM; 4381A51B711D689E CRC64;

Query March 100.0%; Score 96; DB 1; Length 390;
 Best local similarity 100.0%; Pred. No. 1.4e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGPPYIWSL 15
 |||||
 Db 318 HANFCLGPPYIWSL 332

Search completed: June 14, 2005, 15:51:06
 Job time : 81.1923 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2005, 15:35:40 ; Search time 16.7308 Seconds
(without alignments)
86.263 Million cell updates/sec

Title: US-09-831-253F-1

Perfect score: 96

Sequence: 1 HANPCLGPCPYIWSL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : Listing first 45 summaries

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	96	100.0	130	2	148196	transforming growt
2	96	100.0	315	2	A40057	transforming growt
3	96	100.0	390	1	WPHU2	transforming growt
4	96	100.0	390	1	WPM52	transforming growt
5	96	100.0	390	2	A26960	transforming growt
6	96	100.0	390	2	JC4023	transforming growt
7	96	100.0	390	2	A27512	transforming growt
8	96	100.0	390	2	146463	transforming growt
9	96	100.0	390	2	S10219	transforming growt
10	96	100.0	391	2	S01413	transforming growt
11	82	85.4	373	2	A41918	transforming growt
12	77	80.2	412	2	A39489	transforming growt
13	74	77.1	382	2	B61036	transforming growt
14	70	72.9	412	2	A61439	transforming growt
15	70	72.9	413	1	WFXLB2	transforming growt
16	70	72.9	414	1	WPM5B2	transforming growt
17	70	72.9	414	1	WPM5B2	transforming growt
18	70	72.9	414	1	A31249	transforming growt
19	70	72.9	442	2	B31249	transforming growt
20	64	66.7	409	2	S01825	transforming growt
21	64	66.7	410	2	A41397	transforming growt
22	64	66.7	410	2	A55706	transforming growt
23	64	66.7	412	2	A36169	transforming growt
24	62	64.6	412	2	A34939	transforming growt
25	49	51.0	360	2	A29619	Vg1 embryonic grow
26	48	50.0	102	2	A36192	inhibin beta-A cha
27	48	50.0	115	2	PM0504	inhibin beta-A cha
28	48	50.0	424	1	B40905	inhibin beta-A cha
29	48	50.0	424	1	S31440	inhibin beta-A cha

30	48	50.0	424	1	WPPGBA	inhibin beta-A cha
31	48	50.0	425	1	S50898	inhibin beta-A cha
32	48	50.0	425	1	I47072	inhibin beta-A cha
33	48	50.0	426	1	B24248	inhibin beta-A cha
34	48	50.0	768	2	T22758	hypothetical prote
35	46	47.9	108	2	D69017	hypothetical prote
36	46	47.9	864	2	JC4624	alpha-glucosidase
37	44	45.8	352	2	JC2466	inhibin beta-C cha
38	44	45.8	399	2	C71728	probable oxygen-in
39	44	45.8	404	2	AB3473	oxygen-independent
40	44	45.8	593	2	F89885	exonuclease ABC s
41	44	45.8	827	2	S48465	6-phosphofructo-2-
42	44	45.8	1382	1	INHUR	insulin receptor p
43	43.5	45.3	239	2	G02630	FcalphaRb - human
44	43.5	45.3	287	2	JH0332	IGa (Fc) receptor,
45	43	44.8	221	2	T20781	hypothetical prote

ALIGNMENTS

```
RESULT 1
148196
transforming growth factor beta-1 precursor - golden hamster (fragment)
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 02-Jul-1996 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004
C:Accession: 148196
R:Wong, D.T.; Donoff, R.B.; Yang, J.; Song, B.Z.; Matossian, K.; Nagura, N.; Elovic, A.;
Am. J. Pathol. 143, 130-142, 1993
A:Title: Sequential expression of transforming growth factors alpha and beta 1 by eosin
A:Reference number: 148196; MUID:93304479; PMID:8317544
A:Accession: 148196
A>Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-130 <RES>
A:Cross-references: UNIPROT:Q08714; EMBL:X60296; NID:g396177; PIDN:CAA42838.1; PID:g3961
C:Superfamily: inhibin

Query Match      100.0%; Score 96; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 HANPCLGPCPYIWSL 15
Db      58 HANPCLGPCPYIWSL 72

RESULT 2
A40057
transforming growth factor beta-1 precursor - bovine (fragment)
N:Alternate names: beta-TGF; cartilage-inducing factor-A; EGF-dependent TGF or dEGF; MGF
C:Species: Bos primigenius taurus (cattle)
C>Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 09-Jul-2004
C:Accession: A40057; A42320; A05284; A24322; B61439
R:Van Obberghen-Schilling, E.; Kondalish, P.; Ludwig, R.L.; Sporn, M.B.; Baker, C.C.
Mol. Endocrinol. 1, 693-698, 1987
A:Title: Complementary deoxyribonucleic acid cloning of bovine transforming growth facto
A:Reference number: A40057; MUID:91042552; PMID:3153459
A:Accession: A40057
A:Molecule type: mRNA
A:Residues: 1-315 <VAN>
A:Cross-references: UNIPROT:P18341; GB:M36271; NID:g163747; PIDN:AAA30778.1; PID:g163748
R:Ogawa, Y.; Schmidt, D.K.; Daesch, J.R.; Chang, R.U.; Glaeser, C.B.
J. Biol. Chem. 267, 2325-2328, 1992
A:Title: Purification and characterization of transforming growth factor-beta2.3 and -be
A:Reference number: A42320; MUID:92129307; PMID:1733936
A:Accession: A42320
A:Molecule type: protein
A:Residues: 204-209, X', 211-217 <OCA>
R:Roberts, A.B.; Anzano, M.A.; Meyers, C.A.; Wideman, J.; Blacher, R.; Pan, Y.C.E.; Stei
Biochemistry 22, 5692-5698, 1983
A:Title: Purification and properties of a type beta transforming growth factor from bovi
A:Reference number: A05284; MUID:84104793; PMID:6607069
```

```

A:Accession: A05284
A:Molecule type: protein
A:Residues: 204-218 <ROB>
R:Sevelin, S.M.; Thompson, A.Y.; Bentz, H.; Rosen, D.M.; McPherson, J.M.; Conti, A.; Sid
U. Biol. Chem. 261, 5693-5695, 1986
A>Title: Cartilage-inducing factor-A. Apparent identity to transforming growth factor-be
A:Reference number: A24322; MUID:86195954; PMID:3754555
A:Accession: A24322
A:Molecule type: protein
A:Residues: 204-233 <SEV>
R:Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.
U. Protein Chem. 10, 565-575, 1991
A>Title: Separation, purification, and sequence identification of TGF-beta1 and TGF-beta
A:Reference number: A61439; MUID:92189724; PMID:1799413
A:Accession: B61439
A:Molecule type: protein
A:Residues: 204-209, 'X', 211-217, 'XX', 220-232 <JIN>
C:Comment: This polypeptide is composed of two polypeptide chains cross-linked by disulf
C:Comment: Type II TGF does not bind to the EGF receptor and lacks intrinsic mitogenic a
ion. Cells grown in monolayer do not respond in a similar manner to these growth factors
C:Superfamily: Inhibin
C:Keywords: glycoprotein; growth factor; heterodimer
F:204-315/Product: transforming growth factor beta-1 #status experimental <MAT>
F:7,61,101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          100.0%; Score 96; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 HANFCLGPCPYIWSL 15
Db      243 HANFCLGPCPYIWSL 257

RESULT 3
WFMU2
transforming growth factor beta-1 precursor (validated) - human
N:Alternate names: growth-inhibitory factor; TGF type 2; TGF-beta
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1986 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C:Accession: A27513; A01395; A22290; I59664; S53444
R:Derynck, R.; Rhee, L.; Chen, E.Y.; Van Tilburg, A.
Nucleic Acids Res. 15, 3188-3189, 1987
A>Title: Intron-exon structure of the human transforming growth factor-beta precursor ge
A:Reference number: A27513; MUID:87174845; PMID:3470709
A:Accession: A27513
A:Molecule type: DNA
A:Residues: 1-390 <DER>
A:Cross-references: UNIPROT:P01137; GB:X05839; GB:Y00112; NID:937097; PID:CAA29283.1; F
R:Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Eaton, D.H.; Bell, J.R.; Assoian, R.K.; Robert
Nature 316, 701-705, 1985
A>Title: Human transforming growth factor-beta complementary DNA sequence and expression
A:Reference number: A01395; MUID:85296501; PMID:3861940
A:Accession: A01395
A:Molecule type: mRNA
A:Residues: 1-9, 'P', 11-24, 'P', 26-159, 'R', 160-390 <DER>
A:Cross-references: GB:X02812; GB:J05114; NID:937092; PID:CAA26580.1; PID:937093
A>Note: the authors suggest that residues 8-23 could represent the hydrophobic core of a
R:Massague, J.; Ilike, B.
U. Biol. Chem. 260, 2636-2645, 1985
A>Title: Cellular receptors for type beta transforming growth factor. Ligand binding and
A:Reference number: A22290; MUID:85131019; PMID:2982829
A:Accession: A22290
A:Molecule type: protein
A:Residues: 279-285, 'XX', 298-301 <MAS>
R:Urushizaki, Y.; Nitsu, Y.; Terui, T.; Koshida, Y.; Mahara, K.; Kohgo, Y.; Urushizaki,
Tumor Res. 22, 41-55, 1987
A>Title: Cloning and expression of the gene for human transforming growth factor-beta in
A:Reference number: I59664
A:Accession: I59664
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 279-390 <RES>

```

```

A:Cross-references: GB:M38449; NID:9339557; PID:AAA36735.1; PID:9339558
R:Stam, K.; Stewart, A.A.; Qu, G.Y.; Iwata, K.K.; Fenyoe, D.; Chait, B.T.; Marshak, D.R.,
Biochem. J. 305, 87-92, 1995
A>Title: Physical and biological characterization of a growth-inhibitory activity purified
A:Reference number: S53444; MUID:95126934; PMID:7826358
A:Accession: S53444
A:Status: preliminary
A:Molecule type: protein
A:Residues: 279-297 <STA>
C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide
C:GeneticS:
A:Gene: GDB:TCFBL, TCFB
A:Cross-references: GDB:120729; OMIM:190180
A:Map position: 19q13.2-19q13.2
C:Superfamily: Inhibin
C:Keywords: glycoprotein; growth factor; homodimer; mitogen; transformation
F:119-278/Domain: signal sequence #status predicted <SIG>
F:124-246/Region: propeptide #status predicted <PRO>
F:279-390/Product: transforming growth factor beta-1 #status experimental <MAT>
F:82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          100.0%; Score 96; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 HANFCLGPCPYIWSL 15
Db      318 HANFCLGPCPYIWSL 332

RESULT 4
WFMU2
transforming growth factor beta-1 precursor - mouse
N:Alternate names: TGF type 2; TGF-beta
C:Species: Mus musculus (house mouse)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C:Accession: A01396
R:Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Goeddel, D.V.
U. Biol. Chem. 261, 4377-4379, 1986
A>Title: The murine transforming growth factor-beta precursor.
A:Reference number: A01396; MUID:86168129; PMID:3007454
A:Accession: A01396
A:Molecule type: mRNA
A:Residues: 1-390 <DER>
A:Cross-references: UNIPROT:P04202; GB:M13177; NID:9201952; PID:AAA0423.1; PID:9201953
A>Note: the authors suggest that residues 8-23 could represent the hydrophobic core of a
C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide
C:Superfamily: Inhibin
C:Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen; transform
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-278/Domain: propeptide #status predicted <PRO>
F:244-246/Region: cell attachment (R-G-D) motif
F:279-390/Product: transforming growth factor beta-1 #status predicted <MAT>
F:82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          100.0%; Score 96; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 HANFCLGPCPYIWSL 15
Db      318 HANFCLGPCPYIWSL 332

RESULT 5
A26960
transforming growth factor beta-1 precursor - green monkey
C:Species: Cercopithecus aethiops (green monkey, grivet)
C:Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 09-Jul-2004
C:Accession: A26960
R:Sharples, K.; Plooman, G.D.; Rose, T.M.; Twardzik, D.R.; Purchio, A.F.
DNA 6, 239-244, 1987

```

A:Title: Cloning and sequence analysis of simian transforming growth factor-beta cDNA.
A:Reference number: A26960; MUID:87246074; PMID:3474130
A:Accession: A26960
A:Molecule type: mRNA
A:Residues: 1-390 <SHA>
A:Cross-references: UNIPROT:P09533; GB:M16658; NID:G176552; PIDN:AAA53569.1; PID:G176553
C:Superfamily: inhibin
C:Keywords: growth factor
F:1-16/Domains: signal sequence
F:17-390/Product: transforming growth factor beta <SIG>
F:17-390/Product: transforming growth factor beta <status predicted <MAT>

Query Match 100.0%; Score 96; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGCPYIWSL 15
Db 318 HANFCLGCPYIWSL 332

RESULT 6

transforming growth factor beta-1 - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 09-Jul-2004
C:Accession: J04023
R:Manning, A.M.; Auchampach, J.A.; Drony, R.F.; Slightom, J.L.
Gene 155, 307-308, 1995

A:Title: Cloning of a canine cDNA homologous to the human transforming growth factor-beta
A:Reference number: J04023; MUID:95237630; PMID:7721110
A:Accession: J04023

A:Molecule type: mRNA
A:Residues: 1-390 <MAN>

A:Cross-references: UNIPROT:P54831; GB:I34956; NID:G516071; PIDN:AAA51458.1; PID:G516072
C:Comment: This factor plays a multifunctional role as a regulator of mammalian cell growth
C:Genetics:
A:Gene: tgf-beta1
C:Superfamily: inhibin

C:Keywords: growth factor; transforming protein
F:28-390/Product: transforming growth factor beta 1 <status predicted <MAT>

Query Match 100.0%; Score 96; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGCPYIWSL 15
Db 318 HANFCLGCPYIWSL 332

RESULT 7

transforming growth factor beta-1 precursor - pig
N:Alternate names: TGF-beta
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 09-Jul-2004
C:Accession: A27512; A26356; I46557
R:Derynck, R.; Rhee, L.

Nucleic Acids Res. 15, 3187, 1987
A:Title: Sequence of the porcine transforming growth factor-beta precursor.

A:Reference number: A27512; MUID:87174844; PMID:3470708
A:Accession: A27512

A:Molecule type: mRNA
A:Residues: 1-390 <DER>

A:Cross-references: UNIPROT:P07200
R:Chelifeitz, S.; Weatherbee, J.A.; Tsang, M.L.S.; Anderson, J.K.; Mole, J.B.; Lucae, R.;
Cell 48, 409-415, 1987

A:Title: The transforming growth factor-beta system, a complex pattern of cross-reactive
A:Reference number: A30830; MUID:87102890; PMID:2879635
A:Accession: A26356

A:Molecule type: protein
A:Residues: 279-322 <CHE>

R:Kondratiah, P.; Van Obberghen-Schilling, E.; Ludwig, R.L.; Dhar, R.; Sporn, M.B.; Robert

J. Biol. Chem. 263, 18313-18317, 1988

A:Title: cDNA cloning of porcine transforming growth factor-beta 1 mRNA. Evidence for a

A:Reference number: I46657; MUID:89054010; PMID:2461367
A:Accession: I46657

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-390 <KON>

A:Cross-references: GB:M23703; NID:G755044; PIDN:AAA64616.1; PID:G755045
C:Genetics:
A:Gene: TGF-beta-1
C:Superfamily: inhibin
C:Keywords: growth factor

Query Match 100.0%; Score 96; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGCPYIWSL 15
Db 318 HANFCLGCPYIWSL 332

RESULT 8

transforming growth factor beta-1 - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
C:Accession: I46463; S45115
R:Woodall, C.J.; McLaren, L.J.; Watt, N.J.
Gene 150, 371-373, 1994

A:Title: Sequence and chromosomal localization of the gene encoding ovine latent transfo
A:Reference number: I46463; MUID:95121932; PMID:7821809
A:Accession: I46463

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-390 <WOO>

A:Cross-references: UNIPROT:P50414; EMBL:X76916; NID:G496648; PIDN:CAA54242.1; PID:G49666
A>Note: submitted to the EMBL Data Library, December 1993
C:Superfamily: inhibin

Query Match 100.0%; Score 96; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGCPYIWSL 15
Db 318 HANFCLGCPYIWSL 332

RESULT 9

transforming growth factor beta-1 precursor - rat
N:Alternate names: TGF type 2; TGF-beta
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: S10219; P70023; S02267

R:Qian, S.W.; Kondratiah, P.; Roberts, A.B.; Sporn, M.B.
Nucleic Acids Res. 18, 3059, 1990
A:Title: cDNA cloning by PCR of rat transforming growth factor beta-1.

A:Reference number: S10219; MUID:90272425; PMID:2349108
A:Accession: S10219

A:Molecule type: mRNA
A:Residues: 1-390 <QIA>

A:Cross-references: UNIPROT:P17246; EMBL:X52498; NID:G57341; PIDN:CAA36741.1; PID:G57342
R:Okada, F.; Yamaguchi, K.; Ichihara, A.; Nakamura, T.
J. Biochem. 106, 304-310, 1989

A:Title: Purification and structural analysis of a latent form of transforming growth fa
A:Reference number: P70023; MUID:90036779; PMID:2478527
A:Accession: P70023

A:Molecule type: protein
A:Residues: 30-32, 'X', 34-38, 'Q', 40-42, 'X', 44 <OKA>
R:Okada, F.; Yamaguchi, K.; Ichihara, A.; Nakamura, T.
FEBS Lett. 242, 240-244, 1989

A>Title: One of two subunits of masking protein in latent TGF-beta is a part of pro-TGF-
A:Reference number: S02267; MUID:89121078; PMID:2914605
A:Accession: S02267
A:Molecule type: protein
A:Residues: 30-32,'X','34-38','Q','40-42','X','44 <OK2>
C:Superfamily: Inhibin
C:Keywords: glycoprotein; growth factor; integrin binding
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-278/Domain: propeptide #status experimental <PRO>
F:244-246/Region: cell attachment (R-G-D) motif
F:279-390/Product: transforming growth factor beta-1 #status predicted <MAT>
F:82,136,176/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 96; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 8,3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGPCPYIWSL 15
Db 318 HANFCLGPCPYIWSL 332

RESULT 10
S01413
transforming growth factor beta-1 precursor - chicken
C:Species: Gallus gallus (chicken)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: S01413
R:Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.
Nucleic Acids Res. 16, 8730, 1988
A>Title: Nucleotide sequence of chicken transforming growth factor-beta 1 (TGF-beta 1).
A:Reference number: S01413; MUID:8835639; PMID:3166520
A:Accession: S01413
A:Molecule type: DNA
A:Residues: 1-391 <JAK>
A:Cross-references: UNIPROT:P07200; EMBL:X12373; NID:963808; PIDN:CAA30933.1; PID:963805
C:Superfamily: Inhibin
C:Keywords: growth factor

Query Match 100.0%; Score 96; DB 2; Length 391;
Best Local Similarity 100.0%; Pred. No. 8,3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGPCPYIWSL 15
Db 319 HANFCLGPCPYIWSL 333

RESULT 11
A41918
transforming growth factor beta-4 precursor - chicken (fragment)
N:Alternate names: TGF-beta 4
C:Species: Gallus gallus (chicken)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A41918; A34941; S03110
R:Burt, D.W.; Jakowlew, S.B.
Mol. Endocrinol. 6, 989-992, 1992
A>Title: Correction: a new interpretation of a chicken transforming growth factor-beta 4
A:Reference number: A41918; MUID:92357039; PMID:1353860
A:Accession: A41918
A:Molecule type: mRNA
A:Residues: 1-373 <BUR>
A:Cross-references: UNIPROT:P09531; GB:M31160; GB:X08012; GB:S41706; NID:91262437; PIDN:
A>Note: sequence extracted from NCBI backbone (NCBI:110186, NCBI:P:110187)
R:Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.
Mol. Endocrinol. 2, 1186-1195, 1988
A>Title: Complementary deoxyribonucleic acid cloning of a messenger ribonucleic acid end
A:Reference number: A34941; MUID:89112198; PMID:2464131
A:Accession: A34941
A:Molecule type: mRNA
A:Residues: 1-382 <KON>
A:Cross-references: UNIPROT:P16176; GB:J05180; NID:9214821; PIDN:AAA49968.1; PID:9214822
R:Roberts, A.B.; Rosa, F.; Roche, N.S.; Colligan, J.E.; Garfield, M.; Rebbert, M.L.; Kondr
A:Cross-references: EMBL:X08012

A>Note: this sequence has been corrected in A41918
C:Superfamily: Inhibin
C:Keywords: glycoprotein; growth factor
F:1/Domain: signal sequence (fragment) #status predicted <SIG>
F:223-225/Region: cell attachment (R-G-D) motif
F:260-373/Product: transforming growth factor beta-4 #status predicted <MAT>
F:54,109,153/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 85.4%; Score 82; DB 2; Length 373;
Best Local Similarity 92.3%; Pred. No. 9,3e-05;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ANFCLGPCPYIWS 14
Db 302 ANFCLGPCPYIWS 314

RESULT 12
A39489
transforming growth factor beta-2 precursor - chicken
N:Alternate names: TGF-beta2
C:Species: Gallus gallus (chicken)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C:Accession: A39489; A61018; S25849
R:Burt, D.W.; Paton, I.R.
DNA Cell Biol. 10, 723-734, 1991
A>Title: Molecular cloning and primary structure of the chicken transforming growth factor
A:Reference number: A39489; MUID:92075163; PMID:1663775
A:Accession: A39489
A:Molecule type: DNA
A:Residues: 1-412 <BUR>
A:Cross-references: UNIPROT:P30371; GB:X58071; NID:963810; PIDN:CAA41101.1; PID:9833616;
R:Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.
Growth Factors 2, 123-133, 1990
A>Title: Complementary deoxyribonucleic acid cloning of an mRNA encoding transforming gr
A:Reference number: A61018; MUID:90253805; PMID:2340183
A:Accession: A61018
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-94,'G','96-244','L',246-412 <JAK>
C:Genetics: 115/1, 169/3, 214/1, 251/1, 309/2, 360/3
A:Initrons: 115/1, 169/3, 214/1, 251/1, 309/2, 360/3
C:Keywords: growth factor; growth regulation; mitogen; transformation
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-300/Domain: propeptide #status predicted <PRO>
F:301-412/Product: transforming growth factor beta-2 #status predicted <MAT>

Query Match 80.2%; Score 77; DB 2; Length 412;
Best Local Similarity 78.6%; Pred. No. 0.00055;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 HANFCLGPCPYIWS 14
Db 340 HANFCLGPCPYIWS 353

RESULT 13
B61036
transforming growth factor beta-5 precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: A34929; B61036
R:Kondalath, P.; Sando, M.J.; Smith, J.M.; Fielde, A.; Roberts, A.B.; Sporn, M.B.; Melton,
J. Biol. Chem. 265, 1089-1093, 1990
A>Title: Identification of a novel transforming growth factor-beta (TGF-beta5) mRNA in X
A:Reference number: A34929; MUID:90110090; PMID:2235601
A:Accession: A34929
A:Molecule type: mRNA
A:Residues: 1-382 <KON>
A:Cross-references: UNIPROT:P16176; GB:J05180; NID:9214821; PIDN:AAA49968.1; PID:9214822
R:Roberts, A.B.; Rosa, F.; Roche, N.S.; Colligan, J.E.; Garfield, M.; Rebbert, M.L.; Kondr
Growth Factors 2, 135-147, 1990

A>Title: Isolation and characterization of TGF-beta2 and TGF-betas from medium condition
A/Reference number: A61036; MUID:90253806; PMID:2340184
C/Accession: B61036
A/Molecule type: protein
A/Residues: 271-276,'X','278-284','XX','287-299 <ROB>
C/Superfamily: inhibin
C/Keywords: growth factor
F/271-382/Product: transforming growth factor beta-5 #status experimental <MAT>

Query Match 77.1%; Score 74; DB 2; Length 382;
Best Local Similarity 76.6%; Pred. No. 0.0014;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ANFCLGCPYIWSL 15
|||:|||||:
Db 311 ANFCLGNCPIYWSM 324

RESULT 14
A61439
transforming growth factor beta-2 - bovine
N/Alternate names: cartilage-inducing factor B; MGF-a; milk growth factor a
C/Species: Bos primigenius taurus (cattle)
C/Date: 07-Oct-1994 #sequence revision 07-Oct-1994 #text_change 09-Jul-2004
C/Accession: A61439; A25485; B42320; S15389
R/Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.
J. Protein Chem. 10, 565-575, 1991
A>Title: Separation, purification, and sequence identification of TGF-beta1 and TGF-beta
A/Reference number: A61439; MUID:92189724; PMID:1799413
A/Accession: A61439
A/Molecule type: protein
A/Residues: 1-112 <JIN>
A/Cross-references: UNIPROT:P21214
A/Experimental source: milk
R/Seyedin, S.M.; Segarini, P.R.; Rosen, D.M.; Thompson, A.Y.; Bentz, H.; Graycar, J.
J. Biol. Chem. 262, 1946-1949, 1987
A>Title: Cartilage-inducing factor-B is a unique protein structurally and functionally
A/Reference number: A25485; MUID:87137406; PMID:3469199
A/Accession: A25485
A/Molecule type: protein
A/Residues: 1-30 <SEX>
A/Experimental source: bone
R/Ogawa, Y.; Schmidt, D.K.; Daesch, J.R.; Chang, R.J.; Glaeser, C.B.
J. Biol. Chem. 267, 2325-2328, 1992
A>Title: Purification and characterization of transforming growth factor-beta2.3 and -be
A/Reference number: A42320; MUID:92129307; PMID:1733936
A/Accession: B42320
A/Molecule type: protein
A/Residues: 1-6,'X','8-14','XX','17-34 <OGA>
A/Experimental source: bone
R/Cox, D.A.; Buerk, R.R.
Eur. J. Biochem. 197, 353-358, 1991
A>Title: Isolation and characterization of milk growth factor, a transforming-growth-fac
A/Reference number: S15389; MUID:91224126; PMID:2026157
A/Accession: S15389
A/Molecule type: protein
A/Residues: 1-16,'X','19 <COX>
A/Experimental source: milk
C/Superfamily: inhibin
C/Keywords: growth factor; growth regulation; heterodimer; homodimer

Query Match 72.9%; Score 70; DB 2; Length 112;
Best Local Similarity 71.4%; Pred. No. 0.002;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWS 14
:|||||:|||||:
Db 40 NANFCAGACPYLWS 53

RESULT 15
WFXLB2
transforming growth factor beta-2 precursor - African clawed frog

C/Species: Xenopus laevis (African clawed frog)
C/Date: 12-Feb-1993 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C/Accession: S09510; A61036
R/Rebert, M.L.; Bhatia-Dey, N.; David, I.B.
Nucleic Acids Res. 18, 2185, 1990
A>Title: The sequence of TGF-beta2 from Xenopus laevis.
A/Reference number: S09510; MUID:90245678; PMID:2336403
A/Accession: S09510
A/Molecule type: mRNA
A/Residues: 1-413 <REB>
A/Cross-references: UNIPROT:P17247; EMBL:X51817; NID:9414789; PIRN:CAA36116.1; PID:g6513
R/Roberts, A.B.; Rosa, F.; Roche, N.S.; Colligan, J.E.; Garfield, M.; Rebert, M.L.; Kond
Growth Factors 2, 135-147, 1990
A>Title: Isolation and characterization of TGF-beta2 and TGF-betas from medium condition
A/Reference number: A61036; MUID:90253806; PMID:2340184
A/Accession: A61036
A/Molecule type: protein
A/Residues: 302-307,'X','309-315','XX','318-319 <ROB>
C/Superfamily: inhibin
C/Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-301/Domain: propeptide #status predicted <PRO>
F/302-413/Product: transforming growth factor beta-2 #status predicted <MAT>
F/172,140,241/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 72.9%; Score 70; DB 1; Length 413;
Best Local Similarity 71.4%; Pred. No. 0.0059;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWS 14
:|||||:|||||:
Db 341 NANFCAGACPYLWS 354

Search completed: June 14, 2005, 15:52:09
Job time : 17.7308 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: June 14, 2005, 15:51:20 ; Search time 78.4615 Seconds
(without alignments)
73.265 Million cell updates/sec

Title: US-09-831-253F-1
Perfect score: 96
Sequence: 1 HANFCLGPCPYIWSL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubppaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubppaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubppaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubppaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubppaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubppaa/US10F_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubppaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	51	9	US-09-864-761-47871
2	96	100.0	60	10	US-09-791-501-122
3	96	100.0	60	16	US-10-812-642-122
4	96	100.0	70	9	US-09-848-664-9
5	96	100.0	98	14	US-10-187-394-1
6	96	100.0	99	10	US-09-754-831A-48
7	96	100.0	99	17	US-10-671-317-48
8	96	100.0	112	9	US-09-813-271B-2
9	96	100.0	112	15	US-10-366-345-54
10	96	100.0	112	17	US-10-872-198-104
11	96	100.0	113	9	US-09-813-398-13

12	96	100.0	113	16	US-10-826-324-13	Sequence 13, Appl
13	96	100.0	114	9	US-09-389-705-23	Sequence 23, Appl
14	96	100.0	114	9	US-09-813-459-22	Sequence 22, Appl
15	96	100.0	114	13	US-10-115-406-21	Sequence 21, Appl
16	96	100.0	114	14	US-10-154-333-23	Sequence 23, Appl
17	96	100.0	114	16	US-10-704-223-21	Sequence 21, Appl
18	96	100.0	115	9	US-09-859-211-47	Sequence 47, Appl
19	96	100.0	115	9	US-09-880-708-25	Sequence 25, Appl
20	96	100.0	115	10	US-09-872-856-47	Sequence 47, Appl
21	96	100.0	115	14	US-10-335-483-29	Sequence 29, Appl
22	96	100.0	115	15	US-10-463-973-47	Sequence 47, Appl
23	96	100.0	115	15	US-10-693-536-19	Sequence 19, Appl
24	96	100.0	115	16	US-10-758-210-19	Sequence 19, Appl
25	96	100.0	139	13	US-10-002-278-8	Sequence 8, Appl
26	96	100.0	185	16	US-10-781-866-52	Sequence 52, Appl
27	96	100.0	218	16	US-10-781-866-51	Sequence 51, Appl
28	96	100.0	315	10	US-09-214-592-25	Sequence 25, Appl
29	96	100.0	390	9	US-09-756-283A-23	Sequence 23, Appl
30	96	100.0	390	10	US-09-214-592-20	Sequence 20, Appl
31	96	100.0	390	10	US-09-214-592-23	Sequence 23, Appl
32	96	100.0	390	10	US-09-214-592-26	Sequence 26, Appl
33	96	100.0	390	10	US-09-214-592-28	Sequence 28, Appl
34	96	100.0	390	10	US-09-214-592-29	Sequence 29, Appl
35	96	100.0	390	10	US-09-214-592-33	Sequence 33, Appl
36	96	100.0	390	14	US-10-087-268-2	Sequence 2, Appl
37	96	100.0	390	14	US-10-087-268-5	Sequence 5, Appl
38	96	100.0	390	14	US-10-087-268-1	Sequence 1, Appl
39	96	100.0	390	15	US-10-131-985-13	Sequence 13, Appl
40	96	100.0	390	15	US-10-366-345-46	Sequence 46, Appl
41	96	100.0	390	16	US-10-746-545-38	Sequence 38, Appl
42	96	100.0	390	16	US-10-688-845-12	Sequence 12, Appl
43	96	100.0	390	17	US-10-741-600-1307	Sequence 1307, Ap
44	96	100.0	390	17	US-10-741-600-1308	Sequence 1308, Ap
45	96	100.0	390	17	US-10-901-417-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-864-761-47871
Sequence 47871, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmca-x-1
CURRENT APPLICATION NUMBER: US/09/864, 761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 47871
LENGTH: 51
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC011462.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.8
OTHER INFORMATION: EST HUMAN HIT: BE737006.1, EVALUE 4.00e-28
OTHER INFORMATION: SWISSPROT HIT: O19011, EVALUE 3.00e-29
US-09-864-761-47871

Query Match 100.0%; Score 96; DB 9; Length 51;
Best Local Similarity 100.0%; Pred. No. 6.9e-06; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1 HANFCLGCPYIMSL 15
DB 31 HANFCLGCPYIMSL 45

RESULT 2
US-09-791-301-122
Sequence 122, Application US/09791301
Publication No. US20030064943A1
GENERAL INFORMATION:
APPLICANT: Pagratia, Nikos
APPLICANT: Gold, Larry
APPLICANT: Lochrie, Michael
TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
TITLE OF INVENTION: Inhibitors
FILE REFERENCE: NEX 87/C
CURRENT APPLICATION NUMBER: US/09/791,301
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 09/046,247
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: 08/458,424
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: 07/714,131
PRIOR FILING DATE: 1991-06-10
PRIOR APPLICATION NUMBER: 07/931,473
PRIOR FILING DATE: 1992-08-17
PRIOR APPLICATION NUMBER: 07/964,624
PRIOR FILING DATE: 1992-10-21
PRIOR APPLICATION NUMBER: 08/117,991
PRIOR FILING DATE: 1993-09-08
PRIOR APPLICATION NUMBER: 07/536,428
PRIOR FILING DATE: 1990-06-11
PRIOR APPLICATION NUMBER: 09/363,939
PRIOR FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 216
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 122

LENGTH: 60
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-791-301-122

Query Match 100.0%; Score 96; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIMSL 15
DB 40 HANFCLGCPYIMSL 54

RESULT 3
US-10-812-642-122
Sequence 122, Application US/10812642
Publication No. US20040258656A1
GENERAL INFORMATION:
APPLICANT: Pagratia, Nikos
APPLICANT: Gold, Larry
APPLICANT: Lochrie, Michael
TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
TITLE OF INVENTION: Inhibitors
FILE REFERENCE: NEX87
CURRENT APPLICATION NUMBER: US/10/812,642
CURRENT FILING DATE: 2004-03-30
PRIOR APPLICATION NUMBER: US/09/363,939A
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: 09/046,247
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: 08/458,424
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: 07/714,131
PRIOR FILING DATE: 1991-06-10
PRIOR APPLICATION NUMBER: 07/931,473
PRIOR FILING DATE: 1992-08-17
PRIOR APPLICATION NUMBER: 07/964,624
PRIOR FILING DATE: 1992-10-21
PRIOR APPLICATION NUMBER: 08/117,991
PRIOR FILING DATE: 1993-09-08
PRIOR APPLICATION NUMBER: 07/536,428
PRIOR FILING DATE: 1990-06-11
NUMBER OF SEQ ID NOS: 216
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 122
LENGTH: 60
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-812-642-122

Query Match 100.0%; Score 96; DB 16; Length 60;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIMSL 15
DB 40 HANFCLGCPYIMSL 54

RESULT 4
US-09-848-664-9
Sequence 9, Application US/09848664
Patent No. US20020146414A1
GENERAL INFORMATION:
APPLICANT: Sakiyama-Eibert, Shelly E.
APPLICANT: Hubbell, Jeffrey A.

TITLE OF INVENTION: Controlled Release of No. US2002014641A1-Heparin Binding Growth
; TITLE OF INVENTION: Factors from Heparin Containing Matrices
; FILE REFERENCE: ETH 108
; CURRENT APPLICATION NUMBER: US/09/848,664
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 09/298,084
; PRIOR FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-848-664-9

Query Match 100.0%; Score 96; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 8.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGCPYIWSL 15
Db 40 HANFCLGCPYIWSL 54

RESULT 5
US-10-187-394-1
; Sequence 1, Application US/10187394
; Publication No. US2003017667A1
; GENERAL INFORMATION:
; APPLICANT: KECK, PETER
; APPLICANT: SMART, JOHN
; TITLE OF INVENTION: SINGLE CHAIN ANALOGS OF TGF-B
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HURWITZ &
; ADDRESS: THIBEAULT, LLP
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/187,394
; FILING DATE: 28-JUNE-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/496,398
; FILING DATE: 02-FEB-2000
; CLASSIFICATION:
; APPLICATION NUMBER: US 08/478,097
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ. EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: STK-059CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7000
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:

NAME/KEY: Protein
; LOCATION: 1..98
; OTHER INFORMATION: /note= "TGF-B1 SEQUENCE"
US-10-187-394-1

Query Match 100.0%; Score 96; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGCPYIWSL 15
Db 26 HANFCLGCPYIWSL 40

RESULT 6
US-09-754-831A-48
; Sequence 48, Application US/09754831A
; Publication No. US20030228345A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Herman
; APPLICANT: Kuberzampath, Thangavel
; APPLICANT: Rueger, David
; APPLICANT: Ozkaynak, Engin
; TITLE OF INVENTION: Osteogenic Devices
; FILE REFERENCE: STK-008CN
; CURRENT APPLICATION NUMBER: US/09/754,831A
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: US 08/375,901
; PRIOR FILING DATE: 1995-01-20
; PRIOR APPLICATION NUMBER: US 08/145,812
; PRIOR FILING DATE: 1993-11-01
; PRIOR APPLICATION NUMBER: US 07/995,345
; PRIOR FILING DATE: 1992-12-22
; PRIOR APPLICATION NUMBER: US 07/315,342
; PRIOR FILING DATE: 1989-02-23
; PRIOR APPLICATION NUMBER: US 07/232,630
; PRIOR FILING DATE: 1988-08-15
; PRIOR APPLICATION NUMBER: US 07/179,406
; PRIOR FILING DATE: 1988-04-08
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 48
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TGF-beta-1
US-09-754-831A-48

Query Match 100.0%; Score 96; DB 10; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGCPYIWSL 15
Db 26 HANFCLGCPYIWSL 40

RESULT 7
US-10-671-317-48
; Sequence 48, Application US/10671317
; Publication No. US20050054825A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Herman
; APPLICANT: Kuberzampath, Thangavel
; APPLICANT: Rueger, David
; APPLICANT: Ozkaynak, Engin
; TITLE OF INVENTION: Osteogenic Devices
; FILE REFERENCE: STK-010C3
; CURRENT APPLICATION NUMBER: US/10/671,317
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US 09/956,582
; PRIOR FILING DATE: 2001-09-19

PRIOR APPLICATION NUMBER: US 09/074,299
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: US 08/417,071
PRIOR FILING DATE: 1995-04-04
PRIOR APPLICATION NUMBER: US 08/145,812
PRIOR FILING DATE: 1993-11-01
PRIOR APPLICATION NUMBER: US 07/995,345
PRIOR FILING DATE: 1989-12-22
PRIOR APPLICATION NUMBER: US 07/315,342
PRIOR FILING DATE: 1989-02-23
PRIOR APPLICATION NUMBER: US 07/232,630
PRIOR FILING DATE: 1988-08-15
PRIOR APPLICATION NUMBER: US 07/179,406
PRIOR FILING DATE: 1988-04-08
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn version 3.3
SEQ ID NO 48
LENGTH: 99
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: TGF-beta-1
US-10-671-317-48

Query Match 100.0%; Score 96; DB 17; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFLGCPPIYWSL 15
Db 26 HANFLGCPPIYWSL 40

RESULT 8

US-09-813-271B-2
Sequence 2, Application US/09813271B
Patent No. US20020115834A1
GENERAL INFORMATION:

APPLICANT:

(A) Nico Cerletti
TITLE OF INVENTION: New process for the production of
biologically active protein

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. US20020115834A1artis Patent Department
STREET: 564 Morris Avenue
CITY: Summit

STATE: New Jersey

COUNTRY: USA

ZIP: 07901

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/813,271B

FILING DATE: 20-Mar-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/02719

FILING DATE: 12-Jul-95

APPLICATION NUMBER: EPO 94810439.3

FILING DATE: 25-Jul-94

ATTORNEY/AGENT INFORMATION:

NAME: Pfeiffer, Henna J.

REGISTRATION NUMBER: 22640

REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 522-6940

TELEFAX: (908) 522-6955

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 112 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-813-271B-2

Query Match 100.0%; Score 96; DB 9; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFLGCPPIYWSL 15
Db 40 HANFLGCPPIYWSL 54

RESULT 9

US-10-366-345-54
Sequence 54, Application US/10366345
Publication No. US20030224501A1
GENERAL INFORMATION:

APPLICANT: Young, et al.

TITLE OF INVENTION: Bone Morphogenetic Protein Polynucleotides, Polypeptides and

FILE REFERENCE: P1189

CURRENT APPLICATION NUMBER: US/10/366,345

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PatentIn version 3.2

SEQ ID NO 54

LENGTH: 112

TYPE: PRT

ORGANISM: Homo sapiens

US-10-366-345-54

Query Match 100.0%; Score 96; DB 15; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFLGCPPIYWSL 15
Db 40 HANFLGCPPIYWSL 54

RESULT 10

US-10-872-198-104
Sequence 104, Application US/10872198
Publication No. US20050002897A1
GENERAL INFORMATION:

APPLICANT: Ulrich HAUPTS

APPLICANT: Andre KOLTERMAN

APPLICANT: Andreas SCHEIDIG

APPLICANT: Christian VOETSMER

TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF

FILE REFERENCE: 04156.000204

CURRENT APPLICATION NUMBER: US/10/872,198

CURRENT FILING DATE: 2004-06-18

PRIOR APPLICATION NUMBER: 60/543,518

PRIOR FILING DATE: 2004-02-11

PRIOR APPLICATION NUMBER: 60/524,960

PRIOR FILING DATE: 2003-11-25

PRIOR APPLICATION NUMBER: EP 04003058

PRIOR FILING DATE: 2004-02-11

PRIOR APPLICATION NUMBER: EP 03025871

PRIOR FILING DATE: 2003-11-11

PRIOR APPLICATION NUMBER: EP 03025851

PRIOR FILING DATE: 2003-11-10

PRIOR APPLICATION NUMBER: EP 03013819

PRIOR FILING DATE: 2003-06-18

NUMBER OF SEQ ID NOS: 149

SOFTWARE: PatentIn version 3.1

SEQ ID NO 104

LENGTH: 112

TYPE: PRT
ORGANISM: Homo sapiens
US-10-872-198-104

Query Match 100.0%; Score 96; DB 17; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWSL 15
DB 40 HANFCLGCPYIWSL 54

RESULT 11
US-09-813-398-13
Sequence 13, Application US/09813398
Patent No. US20020169292A1
GENERAL INFORMATION:
APPLICANT: Bruce D. Weintraub
APPLICANT: Mariusz W. Szkludinski
APPLICANT: University of Maryland
TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
FILE REFERENCE: USFMD.003C1
CURRENT FILING DATE: 2001-03-20
PRIORITY FILING DATE: 1999-03-19
PRIORITY APPLICATION NUMBER: PCT/US99/05908
PRIORITY FILING DATE: 1998-09-22
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 113
TYPE: PRT
ORGANISM: HOMO SAPIEN
US-09-813-398-13

Query Match 100.0%; Score 96; DB 9; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWSL 15
DB 41 HANFCLGCPYIWSL 55

RESULT 12
US-10-826-324-13
Sequence 13, Application US/10826324
Publication No. US20040265972A1
GENERAL INFORMATION:
APPLICANT: Bruce D. Weintraub
APPLICANT: Mariusz W. Szkludinski
APPLICANT: University of Maryland
TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
FILE REFERENCE: USFMD.003C1
CURRENT APPLICATION NUMBER: US/10/826,324
CURRENT FILING DATE: 2004-04-19
PRIORITY FILING DATE: 2001-03-20
PRIORITY FILING DATE: 1999-03-19
PRIORITY APPLICATION NUMBER: PCT/US99/05908
PRIORITY FILING DATE: 1998-09-22
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 113
TYPE: PRT
ORGANISM: HOMO SAPIEN
US-10-826-324-13

Query Match 100.0%; Score 96; DB 16; Length 113;

Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWSL 15
DB 41 HANFCLGCPYIWSL 55

RESULT 13
US-09-389-705-23
Sequence 23, Application US/09389705
Publication No. US20010018509A1
GENERAL INFORMATION:
APPLICANT: JOHNS HOPKINS UNIVERSITY
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/389,705
FILING DATE: 03-Sep-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/153,733
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. Ph.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD2279 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta 1
FEATURE:
NAME/KEY: Protein
LOCATION: 1..114
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-389-705-23

Query Match 100.0%; Score 96; DB 9; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWSL 15
DB 42 HANFCLGCPYIWSL 56

RESULT 14
US-09-813-459-22
Sequence 22, Application US/09813459
Patent No. US20020107369A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-jin
Cunningham, No. US20020107369A1

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,459
FILING DATE: 20-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/624,635
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John R.,
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-3054
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-1
FEATURE:
NAME/KEY: Protein
LOCATION: 1..114
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-813-459-22

Query Match 100.0%; Score 96; DB 9; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWSL 15
|||
Db 42 HANFCLGCPYIWSL 56

RESULT 15
US-10-115-406-21
Sequence 21, Application US/10115406
Publication No. US20020127612A1
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: LEE, Se-Jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
FILE REFERENCE: JHU1190-3
CURRENT APPLICATION NUMBER: US/10/115,406
CURRENT FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: 09/301,520
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: US 09/172,062
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 08/491,835
PRIOR FILING DATE: 1995-10-23
PRIOR APPLICATION NUMBER: PCT/US94/00685
PRIOR FILING DATE: 1994-01-12
PRIOR APPLICATION NUMBER: US 08/003,303
PRIOR FILING DATE: 1993-01-12

NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.0
SEQ ID NO 21
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-115-406-21

Query Match 100.0%; Score 96; DB 13; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWSL 15
|||
Db 42 HANFCLGCPYIWSL 56

Search completed: June 14, 2005, 16:14:52
Job time : 79.4615 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comphen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 12:54:46 ; Search time 136 Seconds

(without alignments)
31.219 Million cell updates/sec

Title: US-09-831-253f-3

Sequence: 1 TSLDATM1WTM 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 35381937 residues

Total number of hits satisfying chosen parameters: 199616

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA:
1: /cgn2_6/ptcdat1/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptcdat1/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptcdat1/pubppa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptcdat1/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptcdat1/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptcdat1/pubppa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptcdat1/pubppa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptcdat1/pubppa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptcdat1/pubppa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptcdat1/pubppa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptcdat1/pubppa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptcdat1/pubppa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptcdat1/pubppa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptcdat1/pubppa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptcdat1/pubppa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptcdat1/pubppa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptcdat1/pubppa/US11_NEW_PUB.pep.*
18: /cgn2_6/ptcdat1/pubppa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptcdat1/pubppa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptcdat1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	46.0	7	9	US-09-758-128-41
2	29	46.0	7	9	US-09-758-128-44
3	29	46.0	7	9	US-09-758-128-41
4	29	46.0	7	9	US-09-758-128-44
5	29	46.0	7	9	US-09-758-128-41
6	29	46.0	7	9	US-09-758-128-44
7	29	46.0	7	9	US-09-758-128-41
8	29	46.0	7	9	US-09-758-128-44
9	29	46.0	7	9	US-09-758-128-41
10	29	46.0	7	9	US-09-758-128-44
11	29	46.0	7	9	US-09-758-128-41
12	29	46.0	7	9	US-09-758-128-44
13	29	46.0	7	9	US-09-758-128-41

14	25	39.7	9	15	US-10-182-252A-632	Sequence 632, App
15	25	39.7	9	15	US-10-182-252A-657	Sequence 657, App
16	25	39.7	9	15	US-10-182-252A-1216	Sequence 1216, App
17	25	39.7	10	14	US-10-200-708-79	Sequence 79, App
18	25	39.7	10	14	US-10-200-708-501	Sequence 501, App
19	25	39.7	11	10	US-09-755-109-7	Sequence 7, App
20	25	39.7	12	9	US-09-823-823-44	Sequence 44, App
21	25	39.7	12	9	US-09-840-277-69	Sequence 69, App
22	25	39.7	12	9	US-09-823-823-44	Sequence 44, App
23	25	39.7	12	9	US-10-609-217-151	Sequence 151, App
24	25	39.7	12	15	US-10-632-388-151	Sequence 151, App
25	25	39.7	12	15	US-10-651-723-151	Sequence 151, App
26	25	39.7	12	15	US-10-645-761-151	Sequence 151, App
27	25	39.7	12	15	US-10-666-696-151	Sequence 151, App
28	25	39.7	12	15	US-10-653-048-151	Sequence 151, App
29	25	39.7	12	15	US-10-651-165-170	Sequence 170, App
30	25	39.7	12	15	US-09-997-209-82	Sequence 82, App
31	25	39.7	12	15	US-10-182-252A-3	Sequence 3, App
32	25	39.7	12	15	US-10-182-252A-215	Sequence 215, App
33	25	39.7	12	15	US-10-182-252A-617	Sequence 617, App
34	25	39.7	12	15	US-10-182-252A-631	Sequence 631, App
35	25	39.7	12	15	US-10-182-252A-656	Sequence 656, App
36	25	39.7	12	15	US-10-182-252A-658	Sequence 658, App
37	25	39.7	12	15	US-10-431-206-82	Sequence 82, App
38	25	39.7	12	15	US-09-809-391-551	Sequence 551, App
39	25	39.7	12	15	US-09-882-171-551	Sequence 551, App
40	25	39.7	12	15	US-10-092-908-58	Sequence 58, App
41	25	39.7	12	15	US-10-164-861-551	Sequence 551, App
42	25	39.7	12	15	US-09-845-042-27	Sequence 27, App
43	25	39.7	12	15	US-10-062-109A-13	Sequence 13, App
44	25	39.7	12	15	US-10-005-460A-13	Sequence 13, App
45	25	39.7	12	15	US-10-182-252A-630	Sequence 630, App

ALIGNMENTS

RESULT 1
US-09-758-128-41
Sequence 41, Application US/09758128
Patent No. US20020107187A1
GENERAL INFORMATION:
APPLICANT: KINGSTON, David J.
APPLICANT: GERRARD, Simon L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
FILE REFERENCE: 016766/0214
CURRENT APPLICATION NUMBER: US/09/758,128
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: AU P19990
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 41
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
US-09-758-128-41
Query Match
Best Local Similarity 46.0%; Score 29; DB 9; Length 7;
Matches 6; Conservative 1; Mismatches 0; Indels 0;
DB 1 TSLDATV 7
RESULT 2
US-09-758-128-44

This page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2005, 15:51:20 ; Search time 73.2308 Seconds
(without alignments)
73.285 Million cell updates/sec

Title: US-09-831-253F-2
Perfect score: 89
Sequence: 1 FCLGPCPYIWSLDT 14

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubppaa/PCTUS_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubppaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubppaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubppaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubppaa/US09A_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubppaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubppaa/US10E_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubppaa/US11A_PUBCOMB.pep:*
- 19: /cgn2_6/ptodata/2/pubppaa/US11A_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*
- 22: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	51	9	US-09-864-761-47871
2	89	100.0	60	10	US-09-791-301-122
3	89	100.0	60	16	US-10-812-642-122
4	89	100.0	70	9	US-09-848-664-9
5	89	100.0	98	14	US-10-187-394-1
6	89	100.0	112	9	US-09-813-271B-2
7	89	100.0	112	15	US-10-366-345-54
8	89	100.0	112	17	US-10-872-198-104
9	89	100.0	113	9	US-09-813-398-13
10	89	100.0	113	16	US-10-826-324-13
11	89	100.0	114	9	US-09-389-705-23

12	89	100.0	114	9	US-09-813-459-22
13	89	100.0	114	13	US-10-115-406-21
14	89	100.0	114	14	US-10-154-333-23
15	89	100.0	114	16	US-10-704-223-21
16	89	100.0	115	9	US-09-859-211-47
17	89	100.0	115	9	US-09-880-708-25
18	89	100.0	115	10	US-09-872-856-47
19	89	100.0	115	14	US-10-335-483-29
20	89	100.0	115	15	US-10-463-973-47
21	89	100.0	115	15	US-10-693-336-19
22	89	100.0	115	16	US-10-758-210-19
23	89	100.0	139	13	US-10-002-278-8
24	89	100.0	185	16	US-10-781-866-52
25	89	100.0	218	16	US-10-781-866-51
26	89	100.0	315	10	US-09-214-592-25
27	89	100.0	390	9	US-09-756-283A-23
28	89	100.0	390	10	US-09-214-592-20
29	89	100.0	390	10	US-09-214-592-23
30	89	100.0	390	10	US-09-214-592-26
31	89	100.0	390	10	US-09-214-592-28
32	89	100.0	390	10	US-09-214-592-29
33	89	100.0	390	10	US-09-214-592-33
34	89	100.0	390	14	US-10-087-268-2
35	89	100.0	390	14	US-10-087-268-5
36	89	100.0	390	14	US-10-276-947-1
37	89	100.0	390	14	US-10-131-585-13
38	89	100.0	390	15	US-10-366-345-46
39	89	100.0	390	16	US-10-746-845-38
40	89	100.0	390	16	US-10-688-845-12
41	89	100.0	390	17	US-10-741-600-1307
42	89	100.0	390	17	US-10-741-600-1308
43	89	100.0	390	17	US-10-901-417-13
44	89	100.0	391	10	US-09-214-592-17
45	89	100.0	391	17	US-10-741-600-1309

ALIGNMENTS

RESULT 1
US-09-864-761-47871
Sequence 47871, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmika-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263, 6
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 47871
LENGTH: 51
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC011462.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.8
OTHER INFORMATION: EST HUMAN HIT: BE737006.1, EVALUE 4.00e-28
OTHER INFORMATION: SWISSPROT HIT: O19011, EVALUE 3.00e-29
US-09-864-761-47871

Query Match 100.0%; Score 89; DB 9; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCLGCPYIWSLDT 14
Db 34 FCLGCPYIWSLDT 47

RESULT 2
US-09-791-301-122
Sequence 122, Application US/09791301
Publication No. US20030064943A1
GENERAL INFORMATION:
APPLICANT: Pagratia, Nikos
APPLICANT: Lochrie, Michael
TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
FILE REFERENCE: NEX 87/C
CURRENT APPLICATION NUMBER: US/09/791,301
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 09/046,247
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: 08/458,424
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: 07/714,131
PRIOR FILING DATE: 1991-06-10
PRIOR APPLICATION NUMBER: 07/931,473
PRIOR FILING DATE: 1992-08-17
PRIOR APPLICATION NUMBER: 07/964,624
PRIOR FILING DATE: 1992-10-21
PRIOR APPLICATION NUMBER: 08/117,991
PRIOR FILING DATE: 1993-09-08
PRIOR APPLICATION NUMBER: 07/536,428
PRIOR FILING DATE: 1990-06-11
PRIOR APPLICATION NUMBER: 09/363,939
PRIOR FILING DATE: 1999-07-25
NUMBER OF SEQ ID NOS: 216
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 122

LENGTH: 60
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-791-301-122

Query Match 100.0%; Score 89; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCLGCPYIWSLDT 14
Db 43 FCLGCPYIWSLDT 56

RESULT 3
US-10-812-642-122
Sequence 122, Application US/10812642
Publication No. US20040258656A1
GENERAL INFORMATION:
APPLICANT: Pagratia, Nikos
APPLICANT: Lochrie, Michael
TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
FILE REFERENCE: NEX87
CURRENT APPLICATION NUMBER: US/10/812,642
PRIOR FILING DATE: 2004-03-30
PRIOR APPLICATION NUMBER: US/09/363,939A
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: 09/046,247
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: 08/458,424
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: 07/714,131
PRIOR FILING DATE: 1991-06-10
PRIOR APPLICATION NUMBER: 07/931,473
PRIOR FILING DATE: 1992-08-17
PRIOR APPLICATION NUMBER: 07/964,624
PRIOR FILING DATE: 1992-10-21
PRIOR APPLICATION NUMBER: 08/117,991
PRIOR FILING DATE: 1993-09-08
PRIOR APPLICATION NUMBER: 07/536,428
PRIOR FILING DATE: 1990-06-11
NUMBER OF SEQ ID NOS: 216
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 122
LENGTH: 60
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-812-642-122

Query Match 100.0%; Score 89; DB 16; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCLGCPYIWSLDT 14
Db 43 FCLGCPYIWSLDT 56

RESULT 4
US-09-848-664-9
Sequence 9, Application US/09848664
Patent No. US2002014641A1
GENERAL INFORMATION:
APPLICANT: Sakiyama-Elbert, Shelly E.
APPLICANT: Hubbell, Jeffrey A.

;; TITLE OF INVENTION: Controlled Release of No. US2002014641A1-Heparin Binding Growth
;; TITLE OF INVENTION: Factors from Heparin Containing Matrices
;; FILE REFERENCE: ETH 108
;; CURRENT APPLICATION NUMBER: US/09/848,664
;; PRIOR FILING DATE: 2001-05-03
;; PRIOR APPLICATION NUMBER: 09/298,084
;; NUMBER OF SEQ ID NOS: 31
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 9
;; LENGTH: 70
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-848-664-9

Query Match 100.0%; Score 89; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPPCPYMSLDT 14
|||
Db 43 FCLGPPCPYMSLDT 56

RESULT 5
US-10-187-394-1
; Sequence 1, Application US/10187394
; Publication No. US20030176667A1
; GENERAL INFORMATION:
; APPLICANT: KECK, PETER
; APPLICANT: SMART, JOHN
; TITLE OF INVENTION: SINGLE CHAIN ANALOGS OF TGF-B
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HURWITZ &
; ADDRESS: THIBEAULT, LLP
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/187,394
; FILING DATE: 28-JUNE-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/496,398
; FILING DATE: 02-FEB-2000
; CLASSIFICATION:
; APPLICATION NUMBER: US 08/478,097
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: STR-059CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7000
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:

;; NAME/KEY: Protein
;; LOCATION: 1..98
;; OTHER INFORMATION: /note="TGF-B1 SEQUENCE"
US-10-187-394-1

Query Match 100.0%; Score 89; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPPCPYMSLDT 14
|||
Db 29 FCLGPPCPYMSLDT 42

RESULT 6
US-09-813-271B-2
; Sequence 2, Application US/09813271B
; Patent No. US20020115834A1
; GENERAL INFORMATION:
; APPLICANT: (A) Nisco Cerletti
; TITLE OF INVENTION: New process for the production of
; biologically active protein
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. US20020115834A1artis Patent Department
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,271B
; FILING DATE: 20-Mar-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/02719
; FILING DATE: 12-Jul-95
; APPLICATION NUMBER: EPO 94810439.3
; FILING DATE: 25-Jul-94
; ATTORNEY/AGENT INFORMATION:
; NAME: Pfeiffer, Henna J.
; REGISTRATION NUMBER: 22640
; REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 522-6940
; TELEFAX: (908) 522-6955
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-813-271B-2

Query Match 100.0%; Score 89; DB 9; Length 112;
Best Local Similarity 100.0%; Pred. No. 6.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPPCPYMSLDT 14
|||
Db 43 FCLGPPCPYMSLDT 56

RESULT 7
US-10-366-345-54
; Sequence 54, Application US/10366345
; Publication No. US2003024501A1

```

; GENERAL INFORMATION:
; APPLICANT: Young, et al.
; TITLE OF INVENTION: Bone Morphogenetic Protein Polynucleotides, Polypeptides and
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: Ptl189
; CURRENT APPLICATION NUMBER: US/10/366,345
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-366-345-54
```

```

Query Match          100.0%; Score 89; DB 15; Length 112;
Best Local Similarity 100.0%; Pred. No. 6.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 FCLGCPYIWSLDT 14
        |||
Db      43 FCLGCPYIWSLDT 56
```

```

RESULT 8
; Sequence 104, Application US/10872198
; Publication No. US2005002897A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHEIDIG
; APPLICANT: Christian VORTSMEIER
; APPLICANT: Ulrich Ketting
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.000204
; CURRENT APPLICATION NUMBER: US/10/872,198
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-198-104
```

```

Query Match          100.0%; Score 89; DB 17; Length 112;
Best Local Similarity 100.0%; Pred. No. 6.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 FCLGCPYIWSLDT 14
        |||
Db      43 FCLGCPYIWSLDT 56
```

```

RESULT 9
; Sequence 13, Application US/09813398
; Patent No. US20020169292A1
; GENERAL INFORMATION:
; APPLICANT: Bruce D. Weintraub
```

```

; APPLICANT: Mariusz W. Skudlinski
; APPLICANT: University of Maryland
; TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
; FILE REFERENCE: UOFMD.003C1
; CURRENT APPLICATION NUMBER: US/09/813,398
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: PCT/US99/05908
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/US98/19772
; PRIOR FILING DATE: 1998-09-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 113
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
US-09-813-398-13
```

```

Query Match          100.0%; Score 89; DB 9; Length 113;
Best Local Similarity 100.0%; Pred. No. 6.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 FCLGCPYIWSLDT 14
        |||
Db      44 FCLGCPYIWSLDT 57
```

```

RESULT 10
; Sequence 13, Application US/10826324
; Publication No. US20040265972A1
; GENERAL INFORMATION:
; APPLICANT: Bruce D. Weintraub
; APPLICANT: Mariusz W. Skudlinski
; APPLICANT: University of Maryland
; TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
; FILE REFERENCE: UOFMD.003C1
; CURRENT APPLICATION NUMBER: US/10/826,324
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US/09/813,398
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: PCT/US99/05908
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/US98/19772
; PRIOR FILING DATE: 1998-09-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 113
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
US-10-826-324-13
```

```

Query Match          100.0%; Score 89; DB 16; Length 113;
Best Local Similarity 100.0%; Pred. No. 6.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 FCLGCPYIWSLDT 14
        |||
Db      44 FCLGCPYIWSLDT 57
```

```

RESULT 11
; Sequence 23, Application US/09389705
; Publication No. US20010018509A1
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
```

CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/389,705
FILING DATE: 03-Sep-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/153,733
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. Ph.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD2279 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta 1
FEATURE:
NAME/KEY: Protein
LOCATION: 1..114
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-389-705-23
Query Match 100.0%; Score 89; DB 9; Length 114;
Best Local Similarity 100.0%; Pred. No. 6.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 FCLGCPYIWSLDT 14
|||
Db 45 FCLGCPYIWSLDT 58
RESULT 12
US-09-813-459-22
Sequence 22, Application US/09813459
Patent No. US20020107369A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
Cunningham, No. US20020107369A1
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESS: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,459
FILING DATE: 20-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/624,635
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John R.,
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-3054
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-1
FEATURE:
NAME/KEY: Protein
LOCATION: 1..114
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-813-459-22
Query Match 100.0%; Score 89; DB 9; Length 114;
Best Local Similarity 100.0%; Pred. No. 6.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 FCLGCPYIWSLDT 14
|||
Db 45 FCLGCPYIWSLDT 58
RESULT 13
US-10-115-406-21
Sequence 21, Application US/10115406
Publication No. US20020127612A1
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
FILE REFERENCE: JH01190-3
CURRENT APPLICATION NUMBER: US/10/115,406
PRIOR FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: 09/301,520
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: US 09/172,062
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 08/491,835
PRIOR FILING DATE: 1995-10-23
PRIOR APPLICATION NUMBER: PCT/US94/00685
PRIOR FILING DATE: 1994-01-12
PRIOR APPLICATION NUMBER: US 08/003,303
PRIOR FILING DATE: 1993-01-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
SEQ ID NO 21
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-115-406-21
Query Match 100.0%; Score 89; DB 13; Length 114;
Best Local Similarity 100.0%; Pred. No. 6.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 FCLGCPYIWSLDT 14
|||
Db 45 FCLGCPYIWSLDT 58
RESULT 14
US-10-154-333-23

```
; Sequence 23, Application US/10154333
; Publication No. US20030109684A1
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/154,333
; FILING DATE: 21-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/389,705
; FILING DATE: 03-Sep-1999
; APPLICATION NUMBER: 09/153,733
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERELL, JR. Ph. D., JOHN R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD2279 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta 1
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..114
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-154-333-23

Query Match 100.0%; Score 89; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 6.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCLGPCPYIWSLDT 14
   |||||
Db 45 FCLGPCPYIWSLDT 58

RESULT 15
US-10-704-223-21
; Sequence 21, Application US/10704223
; Publication No. US20040152143A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; APPLICANT: LEE, Se-jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
; FILE REFERENCE: JH01190-7
; CURRENT APPLICATION NUMBER: US/10/704,223
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 10/115,406
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US 09/301,520
; PRIOR FILING DATE: 1999-04-28
```

```
; PRIOR APPLICATION NUMBER: US 09/172,062
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 08/491,835
; PRIOR FILING DATE: 1995-10-23
; PRIOR APPLICATION NUMBER: PCT/US94/00685
; PRIOR FILING DATE: 1994-01-12
; PRIOR APPLICATION NUMBER: US 08/003,303
; PRIOR FILING DATE: 1993-01-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 21
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-704-223-21

Query Match 100.0%; Score 89; DB 16; Length 114;
Best Local Similarity 100.0%; Pred. No. 6.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCLGPCPYIWSLDT 14
   |||||
Db 45 FCLGPCPYIWSLDT 58

Search completed: June 14, 2005, 16:14:52
Job time : 73.2308 secs
```


XX SQ Sequence 14 AA;

Query Match 100.0%; Score 89; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14
1 FCLGPCPYIWSLDT 14

RESULT 2
ID AAY92946 standard; peptide; 14 AA.
XX AAY92946;

DT 08-NOV-2000 (first entry)

DE Transforming growth factor inhibitory peptide #2.

XX KW Hepatotropic; antagonist; transforming growth factor betal; TGF- β 1;
XX KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX KW extracellular matrix degradation inhibitor; mimotope; cirrhosis.

OS Homo sapiens.

XX PN W0200031135-A1.

XX PD 02-JUN-2000.

XX PF 23-NOV-1999; 99WO-ES000375.

XX PR 24-NOV-1998; 98ES-00002465.

XX PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX PI Ezquerro Saenz J, Lasarte Sagastibelza J, Prieto Valtuena J;
XX PI Borras Cuesta F;

XX DR WPI; 2000-411935/35.

XX PT Peptides that antagonize binding of transforming growth factor betal,
XX PT useful for treatment of liver disease, especially cirrhosis, are partial
XX PT sequences of the factor or its receptors.

XX PS Claim 3; Page 80; 86pp; Spanish.

XX CC The invention relates to synthetic peptides that antagonise the binding
XX CC of transforming growth (TGF) factor betal (TGF- β 1) to its receptor in
XX CC vivo which have partial amino acid sequences identical, or similar, with
XX CC those of TGF- β 1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX CC examples of the peptides of the invention. The peptides act by
XX CC competitive inhibition of the binding of TGF- β 1 to its receptors, e.g.
XX CC they are inhibitors of stimulation of collagen synthesis in liver cells
XX CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX CC expression systems) encoding the peptides are used for treatment of liver
XX CC disease, specifically cirrhosis

XX SQ Sequence 14 AA;

Query Match 100.0%; Score 89; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14
1 FCLGPCPYIWSLDT 14

RESULT 3

AAY92982
ID AAY92982 standard; peptide; 21 AA.

XX AC AAY92982;

XX DT 08-NOV-2000 (first entry)

XX DE Transforming growth factor inhibitory peptide P28.

XX KW Hepatotropic; antagonist; transforming growth factor betal; TGF- β 1;
XX KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX KW extracellular matrix degradation inhibitor; mimotope; cirrhosis.

XX OS Homo sapiens.

XX PN W0200031135-A1.

XX PD 02-JUN-2000.

XX PF 23-NOV-1999; 99WO-ES000375.

XX PR 24-NOV-1998; 98ES-00002465.

XX PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX PI Ezquerro Saenz J, Lasarte Sagastibelza J, Prieto Valtuena J;
XX PI Borras Cuesta F;

XX DR WPI; 2000-411935/35.

XX PT Peptides that antagonize binding of transforming growth factor betal,
XX PT useful for treatment of liver disease, especially cirrhosis, are partial
XX PT sequences of the factor or its receptors.

XX PS Disclosure; Page 24; 86pp; Spanish.

XX CC The invention relates to synthetic peptides that antagonise the binding
XX CC of transforming growth (TGF) factor betal (TGF- β 1) to its receptor in
XX CC vivo which have partial amino acid sequences identical, or similar, with
XX CC those of TGF- β 1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX CC examples of the peptides of the invention. The peptides act by
XX CC competitive inhibition of the binding of TGF- β 1 to its receptors, e.g.
XX CC they are inhibitors of stimulation of collagen synthesis in liver cells
XX CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX CC expression systems) encoding the peptides are used for treatment of liver
XX CC disease, specifically cirrhosis

XX SQ Sequence 21 AA;

Query Match 100.0%; Score 89; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14
1 FCLGPCPYIWSLDT 14

RESULT 4
ID AAY92983 standard; peptide; 23 AA.
XX AAY92983;

XX DT 08-NOV-2000 (first entry)

XX DE Transforming growth factor inhibitory peptide P29.

XX KW Hepatotropic; antagonist; transforming growth factor betal; TGF- β 1;
XX KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX KW extracellular matrix degradation inhibitor; mimotope; cirrhosis.

OS Homo sapiens.
XX W0200031135-A1.
PN 02-JUN-2000.
XX 23-NOV-1999; 99WO-ES000375.
XX 24-NOV-1998; 98ES-00002465.
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX Ezquerro Saenz JI, Lasarte Sagaribelza JU, Prieto Valtuena J;
PI Borras Cuesta F;
XX WPI; 2000-411935/35.
DR Peptides that antagonise binding of transforming growth factor betaf,
XX useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.
PS Disclosure; Page 24; 86pp; Spanish.
XX The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor betaf (TGF-b1) to its receptor in
CC those which have partial amino acid sequences identical, or similar, with
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis
XX
SQ Sequence 23 AA;
Query Match 100.0%; Score 89; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FCLGCPYIWSLDT 14
DB 10 FCLGCPYIWSLDT 23
RESULT 5
ID AAY92954
XX AAY92954 standard; peptide; 23 AA.
XX AAY92954;
XX 08-NOV-2000 (first entry)
XX Transforming growth factor inhibitory peptide #10.
XX Hepatotropic; antagonist; transforming growth factor betaf; TGF-b1;
KM competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KM extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX Homo sapiens.
XX W0200031135-A1.
PN 02-JUN-2000.
XX 23-NOV-1999; 99WO-ES000375.
XX 24-NOV-1998; 98ES-00002465.
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX Ezquerro Saenz JI, Lasarte Sagaribelza JU, Prieto Valtuena J;
PI

PI Borras Cuesta F;
XX WPI; 2000-411935/35.
DR Peptides that antagonise binding of transforming growth factor betaf,
XX useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.
XX Claim 11; Page 82; 86pp; Spanish.
XX The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor betaf (TGF-b1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis
XX
SQ Sequence 23 AA;
Query Match 100.0%; Score 89; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FCLGCPYIWSLDT 14
DB 10 FCLGCPYIWSLDT 23
RESULT 6
ID ABU08659
XX ABU08659 standard; peptide; 25 AA.
XX ABU08659;
XX 09-JUN-2003 (first entry)
XX Human transforming growth factor (TGF)-beta 1 residues 41-65.
XX Human; transforming growth factor beta 1; TGF-betaf;
KM TGF-beta induced growth inhibition; TGF-beta receptor; binding inhibitor;
KM mink lung epithelial cell; incimal hyperplasia; angioplasty;
KM tissue fibrosis; glomerulonephritis.
XX Homo sapiens.
XX US6500920-B1.
XX 31-DEC-2002.
XX 11-JUN-1998; 98US-00095637.
XX 19-JUN-1997; 97US-0050202P.
XX (UYSL-) UNIV ST LOUIS.
XX Haung JS;
XX WPI; 2003-352187/33.
XX New peptides of transforming growth factor-beta 1, 2 and 3 useful for
PT inhibiting specific binding of TGF-beta to its receptor and for blocking
XX TGF-beta induced growth inhibition of a cell.
XX Claim 14; Fig 5B; 14pp; English.
XX The invention describes a peptide (I) of at least 25 amino acids
CC comprising amino acids 49-58 of transforming growth factor (TGF)-beta 2,
CC amino acids 41-65 of TGF-beta 1, or amino acids 41-65 of TGF-beta 3

CC capable of blocking TGF-beta induced growth inhibition of a cell. The TGF
CC -beta 2 and TGF-beta 1 are also capable of inhibiting specific binding of
CC TGF-beta to TGF-beta receptor on a cell. The methods are useful for
CC inhibiting specific binding of a TGF-beta to a TGF-beta receptor on a
CC cell comprising contacting the cell with a peptide of 10-25 amino acids,
CC where: (a) the peptide comprises amino acids 49-58 of a TGF-beta 1 or
CC amino acids 49-58 of a TGF-beta 2; and (b) the peptide inhibits the
CC specific binding of a TGF-beta to a TGF-beta receptor on a cell. The
CC methods are also useful for blocking TGF-beta-induced growth inhibition
CC of a cell comprising contacting the cell with a peptide of at least 10
CC amino acids, as described above, in particular a mink lung epithelial
CC cell. The methods are also useful for blocking TGF-beta-induced growth
CC inhibition of a cell comprising contacting the cell with a peptide of at
CC least 25 amino acids, where: (a) the peptide comprises amino acids 41-65
CC of a TGF-beta 1, or amino acids 41-65 of a TGF-beta 2; and (b) the
CC peptide blocks TGF-beta-induced growth inhibition of the cell. The
CC peptides are useful in inhibiting, ameliorating or reversing the effects
CC of TGF-beta and treating diseases in which TGF-beta is associated such as
CC intimal hyperplasia, following angioplasty, tissue fibrosis and
CC glomerulonephritis. This is the amino acid sequence of human transforming
CC growth factor (TGF)-beta 1 residues 41-65
XX

SQ Sequence 25 AA;

Query Match 100.0%; Score 89; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14
| | | | | | | | | | | | | | | |
Db 3 FCLGPCPYIWSLDT 16

RESULT 7

ID AAM79533 standard; peptide: 25 AA.

AC AAM79533;

DT 22-APR-2004 (first entry)

DE Human transforming growth factor betal peptide.

XX Human; TGF beta; transforming growth factor beta; antagonist;

XX cutaneous wound; burn; wound healing; vulnary; nephrotoxic;

XX ophthalmological; cytostatic; antiinflammatory; hepatotropic; cardiant.

XX Homo sapiens.

XX MO2003093293-A2.

XX 13-NOV-2003.

XX 15-APR-2003; 2003WO-US011437.

XX 29-APR-2002; 2002US-00135946.

XX (YUSL-) UNIV SAINT LOUIS.

XX Huang JS;

XX WPI; 2004-042374/04.

XX Inhibiting activity of transforming growth factor-beta useful for
XX treating wounds, cancer or fibrosis, comprises administering composition
XX comprising peptide antagonist of transforming growth factor-beta.

XX Claim 4; Fig 5B; ODP; English.

XX The present invention relates to a method of inhibiting activity of
XX transforming growth factor-beta (TGF-beta), which comprises administering
XX a composition comprising a non-naturally occurring peptide that binds to
XX a TGF-beta receptor, blocks the TGF-beta receptor from binding naturally

CC occurring TGF-beta and inhibits the activity of TGF-beta. The method can
CC be used for reducing scarring due to wounds, such as burns, scrapes,
CC puncture wounds and lacerations, promoting re-epithelialization of a
CC wound, reducing the deposition of an extracellular matrix protein in the
CC extracellular matrix and treating diseases mediated by TGF-beta activity,
CC particularly glomerulonephritis, macular degeneration, intimal
CC hyperplasia, cancer, fibrosis (e.g. scar formation, liver cirrhosis, and
CC kidney fibrosis), cystic fibrosis, lung fibrosis or heart fibrosis) and
CC respiratory distress syndrome. The present sequence is a fragment of the
CC human TGF betal protein
XX

SQ Sequence 25 AA;

Query Match 100.0%; Score 89; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14
| | | | | | | | | | | | | | | |
Db 3 FCLGPCPYIWSLDT 16

RESULT 8

ID AAR90828 standard; peptide: 50 AA.

AC AAR90828;

DT 25-MAR-2003 (revised)

DT 25-JAN-1980 (first entry)

DE Pre-transforming growth factor beta 1 residues 252 to 302.

XX transforming growth factor beta 1; wound healing; recombinant production.

XX Homo sapiens.

XX US5482851-A.

XX 09-JAN-1996.

XX 05-NOV-1993; 93US-00147364.

XX 22-MAR-1985; 85US-00715142.

XX 13-MAR-1987; 87US-00025423.

XX 04-AUG-1989; 89US-00389929.

XX 04-MAR-1992; 92US-00845893.

XX (GETH) GENENTECH INC.

XX Goeddel DV, Derynck RMA;

XX WPI; 1996-076891/08.

XX N-PSDB; AAT15721.

XX New recombinant human transforming growth factor-beta prods. - produced
XX using Chinese hamster ovary cells, for use in diagnostic applications or
XX in therapy.

XX Example 2; Fig 2; 26pp; English.

XX The transforming growth factor (TGF) beta 1 exon (residues 252 to 302)
XX was identified using the "long probe" strategy used previously for TGF-
XX alpha. Long oligonucleotides (71572-23) designed on the basis of the
XX partial protein sequence were used as hybridisation probes for the exon
XX in a human genomic DNA library. The TGF beta 1 exon was then used as a
XX probe for the isolation of TGF beta 1 cDNA (see AAT15270). DNA encoding
XX TGF beta 1 is useful for the recombinant production of the protein, which
XX is useful in, e.g. wound healing. (Updated on 25-MAR-2003 to correct PF
XX field.)

SQ Sequence 50 AA;

Query Match 100.0%; Score 89; DB 2; Length 50;
 Best Local Similarity 100.0%; Pred. No. 3.1e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIMSLDT 14
 |||||
 DB 34 FCLGPCPYIMSLDT 47

RESULT 9
 AAR04075
 ID AAR04075 standard; protein, 51 AA.
 AC AAR04075;
 XX
 XX 25-MAR-2003 (revised)
 DT 31-OCT-2002 (revised)
 DT 31-MAY-1989 (first entry)
 XX
 DE Sequence of genomic fragment encoding a TGF-beta 1 exon.
 XX
 XX Transforming growth factor beta-3 (TGF beta 3); tumour cells;
 KM growth inhibition.
 XX
 XX Homo sapiens.
 OS
 XX W08912101-A.
 PN
 XX 14-DEC-1989.
 PD
 XX 08-JUN-1988; 88WO-US001945.
 PF
 XX 08-JUN-1988; 88WO-US001945.
 XX
 PR 08-JUN-1988; 88WO-US001945.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Derynck RMA, Goeddel DV;
 PI
 XX WPI; 1990-007474/01.
 DR P-PSDB; AAR04075.
 XX
 XX Nucleotide sequence encoding transforming growth factor beta-3 - used as
 PT a probe, or to produce tgf beta-3, for growth inhibition of certain
 PT normal and neoplastic cells, e.g. A549.
 XX
 XX Disclosure; Fig 2; 61pp; English.
 PS
 XX This sequence encodes an exon of transforming growth factor-beta 1 (TGF-
 CC beta 1) polypeptide corresponding to AA's 288-338 of mature TGF-beta 1.
 CC The nucleic acid sequence encoding the second subtype of TGF-beta (TGF-
 CC beta 3) is useful as a probe or to produce TGF-beta 3 for both normal and
 CC neoplastic cell growth inhibition. (Updated on 31-OCT-2002 to add missing
 CC OS field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-
 CC MAR-2003 to correct PI field.)
 CC
 SQ Sequence 51 AA;

Query Match 100.0%; Score 89; DB 2; Length 51;
 Best Local Similarity 100.0%; Pred. No. 3.2e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIMSLDT 14
 |||||
 DB 34 FCLGPCPYIMSLDT 47

RESULT 10
 AAW78788
 ID AAW78788 standard; protein, 51 AA.
 AC AAW78788;
 XX
 XX 25-MAR-2003 (revised)

DT 21-DEC-1998 (first entry)
 XX
 XX Human transforming growth factor-beta fragment (aa288-338).
 DE
 XX Transforming growth factor-beta 1; TGF-beta 1; human.
 KM
 XX Homo sapiens.
 OS
 XX US5801231-A.
 PN
 XX 01-SEP-1998.
 PD
 XX 30-MAY-1995; 95US-00454468.
 PF
 XX 22-MAR-1985; 85US-00715142.
 PR 13-MAR-1987; 87US-00025423.
 PR 04-AUG-1989; 89US-00389929.
 PR 04-MAR-1992; 92US-00845893.
 PR 05-NOV-1993; 93US-00147364.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Derynck RMA, Goeddel DV;
 PI
 XX WPI; 1998-494840/42.
 DR N-PSDB; AAV52936.
 XX
 XX DNA encoding transforming growth factor-beta precursor sequence - useful
 PT for analysis to perform manipulations to increase yield of recombinant
 PT production of the protein.
 XX
 XX Example 2; Fig 2; 26pp; English.
 PS
 XX This polypeptide comprises amino acid residues 288-338 of human
 CC transforming growth factor-beta 1 precursor (preTGF-beta 1, see also
 CC AAW78785). It is encoded by an isolated fragment (see AAV52936) of the
 CC TGF-beta 1 gene. The invention relates to the recombinant production of
 CC TGF-beta. Nucleic acid encoding TGF-beta have been isolated and cloned
 CC into vectors which are replicated in bacteria and expressed in eukaryotic
 CC cells. TGF-beta recovered from transformed cells is used in known
 CC therapeutic applications. (Updated on 25-MAR-2003 to correct PR field.)
 CC
 SQ Sequence 51 AA;

Query Match 100.0%; Score 89; DB 2; Length 51;
 Best Local Similarity 100.0%; Pred. No. 3.2e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIMSLDT 14
 |||||
 DB 34 FCLGPCPYIMSLDT 47

RESULT 11
 ABB43879
 ID ABB43879 standard; peptide, 51 AA.
 AC ABB43879;
 XX
 XX 04-FEB-2002 (first entry)
 DT
 XX Peptide #11385 encoded by human foetal liver single exon probe.
 DE
 XX Human; foetal liver; gene expression; single exon nucleic acid probe.
 KM
 XX Homo sapiens.
 OS
 XX W0200157277-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 30-JAN-2001; 2001WO-US000669.
 PF
 XX

PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
PS Claim 27; SEQ ID NO 36514; 639bp + Sequence Listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 51 AA;
XX
Query Match 100.0%; Score 89; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FCLGPCPYIWSLDT 14
Db 34 FCLGPCPYIWSLDT 47
XX
RESULT 12
AAM37799
ID AAM37799 standard; protein; 51 AA.
XX
AC AAM37799;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #11836 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KM genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488897/53.

XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
PS Claim 27; SEQ ID NO 38068; 654bp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SEQ:
CC see A113115-A157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
SQ Sequence 51 AA;
XX
Query Match 100.0%; Score 89; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FCLGPCPYIWSLDT 14
Db 34 FCLGPCPYIWSLDT 47
XX
RESULT 13
AAM7605
ID AAM7605 standard; protein; 51 AA.
XX
AC AAM7605;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 37911.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000668.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
XX
PS Example 4; SEQ ID NO 37911; 658bp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is a
CC protein encoded by one of the probes of the invention
XX
SQ Sequence 51 AA;

CC diagnostics, imaging agents and immunohistochemical reagents
XX
SQ Sequence 60 AA;

Query Match 100.0%; Score 89; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPPYIWSLDT 14
| | | | | | | | | |
Db 43 FCLGPPYIWSLDT 56

Search completed: June 14, 2005, 15:46:23
Job time : 80.2308 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2005, 15:35:40 ; Search time 15.6154 Seconds
(without alignments)
86.263 Million cell updates/sec

Title: US-09-831-253F-2
Perfect score: 89
Sequence: 1 FCLGCPPIWSLDT 14

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	130	2	I48196 transforming growt
2	89	100.0	315	2	A40057 transforming growt
3	89	100.0	390	1	WPHU2 transforming growt
4	89	100.0	390	1	WPHU2 transforming growt
5	89	100.0	390	1	WPHU2 transforming growt
6	89	100.0	390	2	A26960 transforming growt
7	89	100.0	390	2	JC4023 transforming growt
8	89	100.0	390	2	A27512 transforming growt
9	89	100.0	390	2	I46463 transforming growt
10	89	100.0	390	2	S10219 transforming growt
11	82	92.1	373	2	S01413 transforming growt
12	75	84.3	382	2	A41918 transforming growt
13	68	76.4	112	2	B61036 transforming growt
14	68	76.4	112	2	A61439 transforming growt
15	68	76.4	412	2	A39489 transforming growt
16	68	76.4	413	1	WFXLB2 transforming growt
17	68	76.4	414	1	WFXLB2 transforming growt
18	68	76.4	414	1	WFXLB2 transforming growt
19	68	76.4	414	2	B31249 transforming growt
20	62	69.7	409	2	S01825 transforming growt
21	62	69.7	410	2	A41397 transforming growt
22	62	69.7	412	2	A34939 transforming growt
23	62	69.7	412	2	A36169 transforming growt
24	61	68.5	410	2	A55706 transforming growt
25	48	51.7	768	2	T22758 transforming growt
26	46	49.4	433	2	D68017 transforming growt
27	44	49.4	433	2	B90288 transforming growt
28	44	49.4	433	2	H90359 transforming growt
29	44	49.4	1382	1	INHUR transforming growt

30	43	48.3	695	2	S66662 protein-glutamine
31	43	48.3	1372	2	A34157 insulin receptor p
32	43	48.3	1383	2	A36080 insulin receptor p
33	42	47.2	157	2	S14021 hypothetical prote
34	42	47.2	239	2	G64924 ntc protein homol
35	42	47.2	239	2	F85774 probable oxidoredu
36	42	47.2	239	2	B90926 hypothetical prote
37	42	47.2	549	2	T33517 organic cation tra
38	42	47.2	556	2	S50862 membrane transport
39	42	47.2	567	2	A33974 protein RL1G1.4
40	41	46.1	274	2	C88931 probable ferredoxi
41	41	46.1	366	2	G82970 hypothetical prote
42	41	46.1	398	2	G90225 probable oxygen-in
43	41	46.1	399	2	C71728 oxygen-inde
44	41	46.1	404	2	AE3473 alpha-glucosidase
45	41	46.1	864	2	JC4624

ALIGNMENTS

RESULT 1

I48196 transforming growth factor beta-1 precursor - golden hamster (fragment)
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 02-Jul-1996 #sequence #revision 04-Oct-1996 #text_change 09-Jul-2004
C:Accession: I48196
R:Wong, D.T.; Donoff, R.B.; Yang, J.; Song, B.Z.; Matossian, K.; Nagura, N.; Eljovic, A.;
Am. J. Pathol. 143, 130-142, 1993
A:Title: Sequential expression of transforming growth factors alpha and beta 1 by eosino-
A:Reference number: I48196; MUID:93304479; PMID:8317544
A:Accession: I48196
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-130 <RES>
A:Cross-references: UNIPROT:Q08714; EMBL:X60296; NID:G396177; PIDN:CAA42838.1; PID:G3961
C:Superfamily: inhibin

Query Match 100.0%; Score 89; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGCPPIWSLDT 14
DB 61 FCLGCPPIWSLDT 74

RESULT 2

A40057 transforming growth factor beta-1 precursor - bovine (fragment)
N:Alternate names: beta-NGF; cartilage-inducing factor-A; BGF-dependent TGF or dBGf; MGF
C:Species: Bos primigenius taurus (cattle)
C:Date: 28-Feb-1992 #sequence #revision 28-Feb-1992 #text_change 09-Jul-2004
C:Accession: A40057; A42320; A05284; A24322; B61439
R:Van Oosbergen-Schilling, B.; Kondaiah, P.; Ludwig, R.L.; Sporn, M.B.; Baker, C.C.
Mol. Endocrinol. 1, 693-698, 1987
A:Title: Complementary deoxyribonucleic acid cloning of bovine transforming growth facto
A:Reference number: A40057; MUID:91042552; PMID:3153455
A:Accession: A40057
A:Molecule type: mRNA
A:Residues: 1-315 <VAN>
A:Cross-references: UNIPROT:P18341; GB:M36271; NID:G163747; PIDN:AAA30778.1; PID:G163748
R:Ogawa, Y.; Schmidt, D.K.; Daesch, J.R.; Chang, R.U.; Glaeser, C.B.
J. Biol. Chem. 267, 2325-2328, 1992
A:Title: Purification and characterization of transforming growth factor-beta2.3 and -be
A:Reference number: A42320; MUID:92129307; PMID:1733936
A:Accession: A42320
A:Molecule type: protein
A:Residues: 204-209, 'X', 211-217 <OGA>
R:Roberts, A.B.; Anzano, M.A.; Meyers, C.A.; Wideman, J.; Blacher, R.; Pan, Y.C.E.; Stei
Biochemistry 22, 5692-5698, 1983
A:Title: Purification and properties of a type beta transforming growth factor from bovi
A:Reference number: A05284; MUID:84104793; PMID:6607069

A:Accession: A05284
A:Molecule type: protein
A:Residues: 204-218 <ROB>
R:Sevedin, S.M.; Thompson, A.Y.; Bentz, H.; Rosen, D.M.; McPherson, J.M.; Conti, A.; Sie
J. Biol. Chem. 261, 5693-5695, 1986
A:Title: Cartilage-inducing factor-A. Apparent identity to transforming growth factor-b
A:Reference number: A24322; MUID:86195954; PMID:3754555
A:Accession: A24322
A:Molecule type: protein
A:Residues: 204-233 <SEY>
R:Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.
J. Protein Chem. 10, 565-575, 1991
A:Title: Separation, purification, and sequence identification of TGF-beta1 and TGF-beta
A:Reference number: A61439; MUID:92189724; PMID:1799413
A:Accession: B61439
A:Molecule type: protein
A:Residues: 204-209 'X', '211-217', 'XX', '220-232' <JIN>
C:Comment: This polypeptide is composed of two polypeptide chains cross-linked by disulf
C:Comment: Type II TGF does not bind to the EGF receptor and lacks intrinsic mitogenic a
ion. Cells grown in monolayer do not respond in a similar manner to these growth factors
C:Superfamily: Inhibin
C:Keywords: glycoprotein; growth factor; heterodimer
F:204-315/Product: transforming growth factor beta-1 #status experimental <MAT>
F:7,61,101/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 100.0%; Score 89; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 FCLGPCPYIWSLDT 14
Db 246 FCLGPCPYIWSLDT 259
RESULT 3
WFM2
transforming growth factor beta-1 precursor [validated] - human
N:Alternate names: growth-inhibitory factor; TGF type 2; TGF-beta
C:Species: Homo sapiens (man)
C>Date: 28-Feb-1986 #sequence revision 19-Oct-1995 #text_change 09-Jul-2004
C:Accession: A27513; A01395; A22290; I59664; S53444
R:Derynck, R.; Rhee, L.; Chen, E.Y.; Van Tilburg, A.
Nucleic Acids Res. 15, 3188-3189, 1987
A:Title: Intron-exon structure of the human transforming growth factor-beta precursor ge
A:Reference number: A27513; MUID:87174845; PMID:3470709
A:Accession: A27513
A:Molecule type: DNA
A:Residues: 1-390 <DER>
A:Cross-references: UNIPROT:P01137; GB:X05839; GB:Y00112; NID:G37097; PIDN:CAA29283.1; F
R:Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Eaton, D.H.; Bell, J.R.; Assefian, R.K.; Robert
Nature 316, 701-705, 1985
A:Title: Human transforming growth factor-beta complementary DNA sequence and expression
A:Reference number: A01395; MUID:85296301; PMID:3861940
A:Accession: A01395
A:Molecule type: mRNA
A:Residues: 1-3, 'P', '11-24', 'P', '26-159', 'R', '160-390' <DE2>
A:Cross-references: GB:X02812; GB:J05114; NID:G37092; PIDN:CAA26580.1; PID:G37093
A:Note: the authors suggest that residues 8-23 could represent the hydrophobic core of a
R:Massagué, J.; Like, B.
J. Biol. Chem. 260, 2636-2645, 1985
A:Title: Cellular receptors for type beta transforming growth factor. Ligand binding and
A:Reference number: A22290; MUID:85131019; PMID:2982829
A:Accession: A22290
A:Molecule type: protein
A:Residues: 279-285 'XX', '298-301' <MAS>
R:Urushizaki, Y.; Nitsu, Y.; Terui, T.; Koshida, Y.; Mahara, K.; Kohgo, Y.; Urushizaki,
Tumor Res. 22, 41-55, 1987
A:Title: Cloning and expression of the gene for human transforming growth factor-beta in
A:Reference number: I59664
A:Accession: I59664
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 279-390 <RES>

A:Cross-references: GB:M38449; NID:G339557; PIDN:AAA36735.1; PID:G339558
R:Stam, K.; Stewart, A.A.; Qu, G.Y.; Iwata, K.K.; Fenyo, D.; Chait, B.T.; Marshak, D.R.,
Biochem. J. 305, 87-92, 1995
A:Title: Physical and biological characterization of a growth-inhibitory activity purified
A:Reference number: S53444; MUID:95126934; PMID:7826358
A:Accession: S53444
A:Status: preliminary
A:Molecule type: protein
A:Residues: 279-297 <STA>
C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide
C:Genetics:
A:Gene: GDB:TGFB1, TGFB
A:Cross-references: GDB:120729; OMIM:190180
A:Map position: 19q13.2-19q13.2
C:Superfamily: Inhibin
C:Keywords: glycoprotein; growth factor; homodimer; mitogen; transformation
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-278/Domain: propeptide #status predicted <PRO>
F:244-246/Region: cell attachment (R-G-D) motif
F:279-390/Product: transforming growth factor beta-1 #status experimental <MAT>
F:82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 100.0%; Score 89; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 FCLGPCPYIWSLDT 14
Db 321 FCLGPCPYIWSLDT 334

RESULT 4
WFM2
transforming growth factor beta-1 precursor - mouse
N:Alternate names: TGF type 2; TGF-beta
C:Species: Mus musculus (house mouse)
C>Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text_change 09-Jul-2004
C:Accession: A01396
R:Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Goeddel, D.V.
J. Biol. Chem. 261, 4377-4379, 1986
A:Title: The murine transforming growth factor-beta precursor.
A:Reference number: A01396; MUID:86168129; PMID:3007454
A:Accession: A01396
A:Molecule type: mRNA
A:Residues: 1-390 <DER>
A:Cross-references: UNIPROT:P04202; GB:M13177; NID:G201952; PIDN:AAA40423.1; PID:G201953
A:Note: the authors suggest that residues 8-23 could represent the hydrophobic core of a
C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide
C:Superfamily: Inhibin
C:Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen; transform
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-278/Domain: propeptide #status predicted <PRO>
F:244-246/Region: cell attachment (R-G-D) motif
F:279-390/Product: transforming growth factor beta-1 #status predicted <MAT>
F:82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 100.0%; Score 89; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 FCLGPCPYIWSLDT 14
Db 321 FCLGPCPYIWSLDT 334
RESULT 5
A26960
transforming growth factor beta-1 precursor - green monkey
C:Species: Cercopithecus aethiops (green monkey, grivet)
C>Date: 05-Oct-1988 #sequence revision 05-Oct-1988 #text_change 09-Jul-2004
C:Accession: A26960
R:Sharples, K.; Pichman, G.D.; Rose, T.M.; Twardzik, D.R.; Purchio, A.F.
DNA 6, 239-244, 1987

A:Title: Cloning and sequence analysis of simian transforming growth factor-beta cDNA.
A:Reference number: A26960; MUID:87246074; PMID:3474130
A:Accession: A26960
A:Molecule type: mRNA
A:Residues: 1-390 <SHA>
A:Cross-references: UNIPROT:P09533; GB:M1658; NID:g176552; PIDN:AAA35369.1; PID:g176553
C:Superfamily: inhibin
C:Keywords: growth factor
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-390/Product: transforming growth factor beta #status predicted <MAT>

Query Match 100.0%; Score 89; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCLGPCPYIWSLDT 14
Db 321 FCLGPCPYIWSLDT 334

RESULT 6
JC4023
transforming growth factor beta-1 - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 09-Jul-2004
C:Accession: JC4023
R:Manning, A.M.; Auchampach, J.A.; Drong, R.F.; Slightom, J.L.
Gene 155, 307-308, 1995
A:Title: Cloning of a canine cDNA homologous to the human transforming growth factor-beta
A:Reference number: JC4023; MUID:95237630; PMID:7721110
A:Accession: JC4023
A:Molecule type: mRNA
A:Residues: 1-390 <MAN>
A:Cross-references: UNIPROT:P54831; GB:L34956; NID:G516071; PIDN:AAA51458.1; PID:G516072
C:Comment: This factor plays a multifunctional role as a regulator of mammalian cell growth
C:Genetics:
A:Gene: tgf-beta1
C:Superfamily: inhibin
C:Keywords: growth factor; transforming protein
F:288-390/Product: transforming growth factor beta 1 #status predicted <MAT>

Query Match 100.0%; Score 89; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCLGPCPYIWSLDT 14
Db 321 FCLGPCPYIWSLDT 334

RESULT 7
A27512
transforming growth factor beta-1 precursor - pig
N:Alternate names: TGF-beta
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 09-Jul-2004
C:Accession: A27512; A26356; I46657
R:Derynck, R.; Rhee, L.
Nucleic Acids Res. 15, 3187, 1987
A:Title: Sequence of the porcine transforming growth factor-beta precursor.
A:Reference number: A27512; MUID:87174844; PMID:3470708
A:Accession: A27512
A:Molecule type: mRNA
A:Residues: 1-390 <DER>
A:Cross-references: UNIPROT:P07200
R:Chelifer, S.; Weatherbee, J.A.; Tang, M.L.S.; Anderson, J.K.; Mole, J.E.; Lucas, R.; Cell 48, 409-415, 1987
A:Title: The transforming growth factor-beta system, a complex pattern of cross-reactive
A:Reference number: A26356; MUID:87102890; PMID:2879635
A:Accession: A26356
A:Molecule type: protein
A:Residues: 279-322 <CHR>
R:Kondalish, P.; Van Obberghen-Schilling, E.; Ludwig, R.L.; Dhar, R.; Sporn, M.B.; Robert

J. Biol. Chem. 263, 18313-18317, 1988
A:Title: cDNA cloning of porcine transforming growth factor-beta 1 mRNAs. Evidence for a
A:Reference number: I46657; MUID:89054010; PMID:2461367
A:Accession: I46657
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-390 <KON>
A:Cross-references: GB:M23703; NID:g755044; PIDN:AAA64616.1; PID:g755045
C:Genetics:
A:Gene: TGF-beta-1
C:Superfamily: inhibin
C:Keywords: growth factor

Query Match 100.0%; Score 89; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCLGPCPYIWSLDT 14
Db 321 FCLGPCPYIWSLDT 334

RESULT 8
I46463
transforming growth factor beta-1 - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
C:Accession: I46463; S45115
R:Woodall, C.J.; McLaren, L.J.; Watt, N.U.
Gene 150, 371-373, 1994
A:Title: Sequence and chromosomal localisation of the gene encoding ovine latent transfo
A:Reference number: I46463; MUID:95121932; PMID:7821809
A:Accession: I46463
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-390 <WOO>
A:Cross-references: UNIPROT:P50414; EMBL:X76916; NID:G496648; PIDN:CAA54242.1; PID:G4966
A:Note: submitted to the EMBL Data Library, December 1993
C:Superfamily: inhibin

Query Match 100.0%; Score 89; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCLGPCPYIWSLDT 14
Db 321 FCLGPCPYIWSLDT 334

RESULT 9
S10219
transforming growth factor beta-1 precursor - rat
N:Alternate names: TGF type 2; TGF-beta
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: S10219; PT0023; S02267
R:Qian, S.W.; Kondalish, P.; Roberts, A.B.; Sporn, M.B.
Nucleic Acids Res. 18, 3059, 1990
A:Title: cDNA cloning by PCR of rat transforming growth factor-beta-1.
A:Reference number: S10219; MUID:90272425; PMID:2349108
A:Accession: S10219
A:Molecule type: mRNA
A:Residues: 1-390 <QIA>
A:Cross-references: UNIPROT:P17246; EMBL:X52498; NID:G57341; PIDN:CAA36741.1; PID:G57342
R:Okada, F.; Yamaguchi, K.; Ichihara, A.; Nakamura, T.
J. Biochem. 106, 304-310, 1989
A:Title: Purification and structural analysis of a latent form of transforming growth fa
A:Reference number: PT0023; MUID:90036779; PMID:2478527
A:Accession: PT0023
A:Molecule type: protein
A:Residues: 30-32, 'X', 34-38, 'Q', 40-42, 'X', 44 <OKA>
R:Okada, F.; Yamaguchi, K.; Ichihara, A.; Nakamura, T.
FEBS Lett. 242, 240-244, 1989

A/Title: One of two subunits of masking protein in latent TGF-beta is a part of pro-TGF-
A/Accession: S02267; MUID:89121078; PMID:2914605
A/Accession: S02267
A/Molecule type: protein
A/Residues: 30-32, 'X', 34-38, 'Q', 40-42, 'X', 44 <OK>
C/Superfamily: inhibin
C/Keywords: glycoprotein; growth factor; integrin binding
F/1-29/Domain: signal sequence #status predicted <SIG>
F/30-278/Domain: propeptide #status experimental <PRO>
F/244-246/Region: cell attachment (R-G-D) motif
F/279-390/Product: transforming growth factor beta-1 #status predicted <MAT>
F/82,136,176/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 89; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FCLGCPYIWSLDT 14
Db 321 FCLGCPYIWSLDT 334

RESULT 10
S01413
transforming growth factor beta-1 precursor - chicken
C/Species: Gallus gallus (chicken)
C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C/Accession: S01413
R/Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.
Nucleic Acids Res. 16, 8730, 1988
A/Title: Nucleotide sequence of chicken transforming growth factor-beta 1 (TGF-beta 1).
A/Reference number: S01413; MUID:88335639; PMID:3166520
A/Accession: S01413
A/Molecule type: DNA
A/Residues: 1-391 <JUK>
A/Cross-references: UNIPROT:P07200; EMBL:X12373; NID:963808; PIDN:CAA30933.1; PID:963808
C/Superfamily: inhibin
C/Keywords: growth factor

Query Match 100.0%; Score 89; DB 2; Length 391;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FCLGCPYIWSLDT 14
Db 322 FCLGCPYIWSLDT 335

RESULT 11
A41918
transforming growth factor beta-4 precursor - chicken (fragment)
N/Alternate names: TGF-beta 4
C/Species: Gallus gallus (chicken)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: A41918; A34941; S03110
R/Burt, D.W.; Jakowlew, S.B.
Mol. Endocrinol. 6, 989-992, 1992
A/Title: Correction: a new interpretation of a chicken transforming growth factor-beta 4
A/Reference number: A41918; MUID:92357039; PMID:1355860
A/Accession: A41918
A/Molecule type: mRNA
A/Residues: 1-373 <BU>
A/Cross-references: UNIPROT:P09531; GB:M31160; GB:X08012; GB:S41706; NID:91262437; PIDN:
A/Note: sequence extracted from NCBI backbone (NCBI:110186, NCBI:P:110187)
A/Note: this report corrects and reinterprets the sequence from reference A34941
R/Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.
Mol. Endocrinol. 2, 1186-1195, 1988
A/Title: Complementary deoxyribonucleic acid cloning of a messenger ribonucleic acid enc
A/Reference number: A34941; MUID:89112198; PMID:2464131
A/Accession: A34941
A/Molecule type: mRNA
A/Residues: 'MDPMISIGPSCGSGPMRPCTAPWISGSRRAINSSCSTSSRYRAVGGAL', 122-209, 'D', 211-373 <
A/Cross-references: EMBL:X08012

A/Note: this sequence has been corrected in A41918
C/Superfamily: inhibin
C/Keywords: glycoprotein; growth factor
F/1/Domain: signal sequence (fragment) #status predicted <SIG>
F/223-225/Region: cell attachment (R-G-D) motif
F/260-373/Product: transforming growth factor beta-4 #status predicted <MAT>
F/54,109,153/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 92.1%; Score 82; DB 2; Length 373;
Best Local Similarity 85.7%; Pred. No. 6.4e-05;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 FCLGCPYIWSLDT 14
Db 304 FCMGCPYIWSADT 317

RESULT 12
B61036
transforming growth factor beta-5 precursor - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C/Accession: A34929; B61036
R/Kondalah, P.; Sande, M.J.; Smith, J.M.; Fields, A.; Roberts, A.B.; Sporn, M.B.; Melton,
J. Biol. Chem. 265, 1089-1093, 1990
A/Title: Identification of a novel transforming growth factor-beta (TGF-beta5) mRNA in X
A/Reference number: A34929; MUID:90110090; PMID:2295601
A/Accession: A34929
A/Molecule type: mRNA
A/Residues: 1-382 <KON>
A/Cross-references: UNIPROT:P16176; GB:J05180; NID:9214821; PIDN:AAA49968.1; PID:9214822
R/Roberts, A.B.; Ross, F.; Roche, N.S.; Colligan, J.E.; Garfield, M.; Redbert, M.L.; Kond
Growth Factors 2, 135-147, 1990
A/Title: Isolation and characterization of TGF-beta2 and TGF-beta5 from medium conditio
A/Reference number: A61036; MUID:90255806; PMID:2340184
A/Accession: B61036
A/Molecule type: protein
A/Residues: 271-276, 'X', 278-284, 'XX', 287-299 <ROB>
C/Superfamily: inhibin
C/Keywords: growth factor

Query Match 84.3%; Score 75; DB 2; Length 382;
Best Local Similarity 78.6%; Pred. No. 0.00073;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 FCLGCPYIWSLDT 14
Db 313 YCLGNCPYIWSMDT 326

RESULT 13
A61439
transforming growth factor beta-2 - bovine
N/Alternate names: cartilage-inducing factor B; MGF-a; milk growth factor a
C/Species: Bos primigenius taurus (cattle)
C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C/Accession: A61439; A25485; B42320; S15389
R/Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.
J. Protein Chem. 10, 565-575, 1991
A/Title: Separation, purification, and sequence identification of TGF-beta1 and TGF-beta2
A/Reference number: A61439; MUID:92189724; PMID:1799413
A/Accession: A61439
A/Molecule type: protein
A/Residues: 1-112 <JIN>
A/Cross-references: UNIPROT:P21214
A/Experimental source: milk
J. Seyedin, S.M.; Segarini, P.R.; Rosen, D.M.; Thompson, A.Y.; Bentz, H.; Graycar, J.
J. Biol. Chem. 262, 1946-1949, 1987
A/Title: Cartilage-inducing factor-B is a unique protein structurally and functionally re
A/Reference number: A25485; MUID:87137406; PMID:3469199
A/Accession: A25485
A/Molecule type: protein

A;Residues: 1-30 <SEX>
A;Experimental source: Bone
R;Ogawa, Y.; Schmidt, D.K.; Daesch, J.R.; Chang, R.J.; Glaeser, C.B.
J. Biol. Chem. 267, 2325-2328, 1992
A;Title: Purification and characterization of transforming growth factor-beta2.3 and -b2
A;Reference number: A42330; MUID:92123907; PMID:1733936
A;Accession: B42320
A;Molecule type: protein
A;Residues: 1-6, 'X', 8-14, 'XX', 17-34 <OGA>
A;Experimental source: bone
R;Cox, D.A.; Buerk, R.R.
Eur. J. Biochem. 197, 353-358, 1991
A;Title: Isolation and characterization of milk growth factor, a transforming-growth-fac
A;Reference number: S15389; MUID:9124126; PMID:2026157
A;Accession: S15389
A;Molecule type: protein
A;Residues: 1-16, 'XX', 19 <COX>
A;Experimental source: milk
C;Superfamily: inhibin
C;Keywords: growth factor; growth regulation; heterodimer; homodimer
Query Match 76.4%; Score 68; DB 2; Length 112;
Best Local Similarity 71.4%; Pred. No. 0.0028;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 FCLGPCPYWMSLDT 14
DB 43 FCAGACPYWMSDT 56
RESULT 14
A39489
transforming growth factor beta-2 precursor - chicken
N;Alternate names: TGF-beta2
C;Species: Gallus gallus (chicken)
C;Date: 17-Jul-1992 #sequence revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: A39489; A61018; S25849
R;Burt, D.W.; Paton, I.R.
DNA Cell Biol. 10, 723-734, 1991
A;Title: Molecular cloning and primary structure of the chicken transforming growth fac
A;Reference number: A39489; MUID:92075163; PMID:1683775
A;Accession: A39489
A;Molecule type: DNA
A;Residues: 1-412 <BUR>
A;Cross-references: UNIPROT:P30371; GB:X58071; NID:963810; PIDN:CAA41101.1; PID:9833616;
R;Jakowlew, S.B.; Dillard, P.J.; Sporn, W.B.; Roberts, A.B.
Growth Factors 2, 123-133, 1990
A;Title: Complementary deoxyribonucleic acid cloning of an mRNA encoding transforming gr
A;Reference number: A61018; MUID:90253805; PMID:2340183
A;Accession: A61018
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-94, 'G', 96-244, 'L', 246-412 <JAK>
C;Genetics:
A;Introns: 115/1; 169/3; 214/1; 251/1; 309/2; 360/3
C;Superfamily: inhibin
C;Keywords: growth factor; growth regulation; mitogen; transformation
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-300/Domain: propeptide #status predicted <PRO>
F;301-412/Product: transforming growth factor beta-2 #status predicted <MAT>
Query Match 76.4%; Score 68; DB 2; Length 412;
Best Local Similarity 71.4%; Pred. No. 0.0088;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 FCLGPCPYWMSLDT 14
DB 343 FCAGACPYWMSDT 356
RESULT 15
WFXLB2
transforming growth factor beta-2 precursor - African clawed frog

C;Species: Xenopus laevis (African clawed frog)
C;Date: 12-Feb-1993 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: S09510; A61036
R;Rebert, M.L.; Bhatia-Dey, N.; Dawid, I.B.
Nucleic Acids Res. 18, 2185, 1990
A;Title: The sequence of TGF-beta2 from Xenopus laevis.
A;Reference number: S09510; MUID:90245678; PMID:2336403
A;Accession: S09510
A;Molecule type: mRNA
A;Residues: 1-413 <RFB>
A;Cross-references: UNIPROT:P17247; EMBL:X51817; NID:9414789; PIDN:CAA36116.1; PID:95513
R;Roberts, A.B.; Rosa, F.; Roche, N.S.; Colligan, J.E.; Garfield, M.; Rebert, M.L.; Kond.
Growth Factors 2, 135-147, 1990
A;Title: Isolation and characterization of TGF-beta2 and TGF-betas from medium condition.
A;Reference number: A61036; MUID:90253806; PMID:2340184
A;Accession: A61036
A;Molecule type: protein
A;Residues: 302-307, 'X', 309-315, 'XX', 318-319 <ROB>
C;Superfamily: inhibin
C;Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-301/Domain: propeptide #status predicted <PRO>
F;302-413/Product: transforming growth factor beta-2 #status predicted <MAT>
F;72,140,241/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 76.4%; Score 68; DB 1; Length 413;
Best Local Similarity 71.4%; Pred. No. 0.0088;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 FCLGPCPYWMSLDT 14
DB 344 FCAGACPYWMSDT 357
Search completed: June 14, 2005, 15:52:10
Job time : 16.6154 secs

This Page Blank (nspru)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2005, 15:34:23 ; Search time 74.8462 Seconds

(without alignments)
95.785 Million cell updates/sec

Title: US-09-831-253F-2
Perfect score: 89
Sequence: 1 FCLGCPYIWSLDT 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	50	2 Q28240	Q28240 cervus elap
2	89	100.0	51	2 Q72487	Q72487 homo sapien
3	89	100.0	78	2 Q70316	Q70316 sus scrofa
4	89	100.0	112	2 Q02730	Q02730 oryctolagus
5	89	100.0	124	2 Q95N80	Q95N80 canis famli
6	89	100.0	130	2 Q08714	Q08714 mesocricetu
7	89	100.0	315	1 TGFI_BOVIN	P18341 bos taurus
8	89	100.0	368	2 Q8R4D9	Q8R4D9 sigmodon hi
9	89	100.0	390	1 TGFI_CANFA	P54831 canis famli
10	89	100.0	390	1 TGFI_CANVO	Q921y6 cavia porce
11	89	100.0	390	1 TGFI_CERAE	P09533 cercopithe
12	89	100.0	390	1 TGFI_HORSE	O19011 equus cabal
13	89	100.0	390	1 TGFI_HUMAN	P01137 homo sapien
14	89	100.0	390	1 TGFI_MOUSE	P04202 mus musculu
15	89	100.0	390	1 TGFI_PIG	P07200 sus scrofa
16	89	100.0	390	1 TGFI_RAT	P17246 rattus norv
17	89	100.0	390	1 TGFI_SHEEP	P15041 ovis aries
18	89	100.0	390	2 Q9TUM6	Q9TUM6 equus cabal
19	82	92.1	101	2 Q9R184	Q9R184 meriones un
20	82	92.1	373	1 TGFI_CHICK	P09531 gallus gall
21	75	84.3	382	1 TGFI_CHICK	P16176 xenopus lae
22	69	77.5	62	2 Q90YF4	Q90YF4 pleuronecte
23	69	77.5	77	2 Q90YF8	Q90YF8 oncorhynch
24	69	77.5	88	2 Q90YF7	Q90YF7 oncorhynch
25	69	77.5	91	2 Q9MYZ1	Q9MYZ1 capra hircu
26	69	77.5	361	2 Q98854	Q98854 cyprinus ca
27	69	77.5	411	2 Q7SZV4	Q7SZV4 brachydanio
28	68	76.4	112	2 Q28241	Q28241 cervus elap
29	68	76.4	112	1 TGFI_BOVIN	P21214 bos taurus
30	68	76.4	224	2 Q8CDZ9	Q8CDZ9 mus musculu
31	68	76.4	255	2 Q921T1	Q921T1 mus musculu

32	68	76.4	399	2 Q9ERB7	Q9ERB7 mesocricetu
33	68	76.4	412	1 TGFI_CHICK	P30371 gallus gall
34	68	76.4	413	1 TGFI_XENIA	P17247 xenopus lae
35	68	76.4	414	1 TGFI_CERAE	P61811 cercopithe
36	68	76.4	414	1 TGFI_HUMAN	P61812 homo sapien
37	68	76.4	414	1 TGFI_MOUSE	P27090 mus musculu
38	68	76.4	414	2 Q91VF5	Q91VF5 mus musculu
39	68	76.4	435	1 TGFI_PIG	P09858 sus scrofa
40	68	76.4	442	1 TGFI_RAT	Q07257 rattus norv
41	68	76.4	442	2 Q6T7C3	Q6T7C3 oryctolagus
42	62	69.7	62	2 Q90YF3	Q90YF3 pleuronecte
43	62	69.7	62	2 Q90YF9	Q90YF9 oncorhynch
44	62	69.7	62	2 Q90Z08	Q90Z08 anguilla an
45	62	69.7	88	2 Q90ZE7	Q90ZE7 acipenser b

ALIGNMENTS

```

RESULT 1
Q28240 PRELIMINARY; PRT; 50 AA.
AC Q28240.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Transforming growth factor beta 1 (TGF-beta 1) (Transforming growth
DE factor B1) (Fragment).
GN Name=TGFB1; Synonym=TGF beta-1, TGF-B1;
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervinae; Cervus.
OX NCBI_TaxID=99860;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Antler;
RX MEDLINE=98233260; PubMed=9571767;
RX DOI=10.1002/(SICI)1097-010X(19980501)281:1<36::AID-JE26>3.0.CO;2-D;
RA Francis S.M., Suttie J.M.;
RT "Detection of growth factors and proto-oncogene mRNA in the growing
RT tip of red deer (Cervus elaphus) antler using reverse-transcriptase
RT polymerase chain reaction (RT-PCR).";
RL J. Exp. Zool. 281:36-42(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Wagener A., Bloctner S., Fickel J.;
RT "Detection of growth factors in the testes of roe deer (Capreolus
RT capreolus).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
CC POLYMERIZATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
CC THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
CC REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
CC DERIVATIVES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -!- SUBUNIT: Homodimer; disulfide-linked (by similarity).
CC -!- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; U62110; AAB05256.1; -.
DR EMBL; AF152591; AAF73230.1; -.
DR HSSP; P01137; IKLA.
DR GO; GO:0008083; P: growth factor activity; IEA.
DR GO; GO:0008283; P: cell proliferation; IEA.
DR GO; GO:0000074; P: regulation of cell cycle; IEA.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Glycoprotein; Growth factor; Mitogen.
FT NON_TER 1
FT CHAIN <1 >50 TRANSFORMING GROWTH FACTOR BETA 1.

```

FT	NON TER	50	50	
SO	SEQUENCE	50 AA,	6012 MW,	0DDDAE48C640759F CRC64;
Query Match				
	Best Local Similarity	100.0%;	Score 89;	DB 2;
	Matches	14;	Conservative	0;
			Mismatches	0;
			Indels	0;
			Gaps	0;
OY	1	FCLGPCPYIWSLDT 14		
Db	35	FCLGPCPYIWSLDT 48		
RESULT 2				
Q72487		PRELIMINARY;	PRT;	51 AA.
ID	Q72487			
AC	Q72487;			
DT	01-OCT-2003 (TREMBLrel. 25, Created)			
DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Transforming growth factor beta 1 (Fragment).			
GN	Name=TGFBI;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Vieira A.R., Murray J.C.;			
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: Belongs to the TGF-beta family.			
DR	EMBL; AY330202; AAQ18642.1; --.			
DR	HSSP; P01137; IKLA.			
DR	GO; GO:0008083; F:growth factor activity; IEA.			
DR	InterPro; IPR01839; TGFb.			
DR	Pfam; PF00019; TGF_beta; 1.			
DR	ProDom; PD000357; TGFb; 1.			
DR	SMART; SM00204; TGFBI; 1.			
DR	PROSITE; PS00250; TGF_BETA_1; 1.			
KW	Growth factor.			
FT	NON TER	1		
FT	NON TER	51		
SO	SEQUENCE	51 AA;	6140 MW;	259F4DB23E48A9D0 CRC64;
Query Match				
	Best Local Similarity	100.0%;	Score 89;	DB 2;
	Matches	14;	Conservative	0;
			Mismatches	0;
			Indels	0;
			Gaps	0;
OY	1	FCLGPCPYIWSLDT 14		
Db	34	FCLGPCPYIWSLDT 47		
RESULT 3				
Q70316		PRELIMINARY;	PRT;	78 AA.
ID	Q70316			
AC	Q70316;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	Transforming growth factor beta 1 (Fragment).			
GN	Name=TGFBI;			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxId=96023;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kopczyn M., Stratiil A., Van Poucke M., Bartsenschlager H.,			
RL	Geldermann H., Peelman L.J.;			
RL	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: Belongs to the TGF-beta family.			
DR	EMBL; AJ621785; CAF21862.1; --.			
DR	HSSP; P01137; IKLA.			

DR	GO: GO:0008083; F.growth factor activity; IEA.
DR	InterPro: IPR001939; TGFb.
DR	Pfam: PF00019; TGF_beta; 1.
DR	ProDom: PD000357; TGFb; 1.
DR	SMART: SM00204; TGFB; 1.
DR	PROSITE: PS00250; TGF_BETA_1; 1.
KW	Growth factor.
FT	NON_TER
FT	CHAIN
FT	NON_TER
SQ	SEQUENCE
Query Match	100.0%; Score 89; DB 2; Length 78;
Best Local Similarity	100.0%; Pred. NO. 2.5e-06;
Matches	14; Conservative 0; Mismatches 0; Indels 0; Gaps
Oy	1 FCIGPCPYIWSLDT 14
Dd	27 FCIGPCPYIWSLDT 40
RESULT 4	
ID	002730 PRELIMINARY; PRT; 112 AA.
AC	002730
DT	01-JUL-1997 (TrEMBLrel. 04, Created)
DT	01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Transforming growth factor beta 1 (TGF-beta 1) (Fragment).
GN	Name=TGFB1; Synonyms=TGF-beta-1; Oryctolagus cuniculus (Rabbit).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI	TaxID=9986; [1]
RP	SEQUENCE FROM N.A.
RA	Taylor T.K., James E.R., McGonigle S., Yoho E.R.;
RL	Submitted (APR-1997) to the EMBL/Genbank/DBJ databases. [2]
RN	RA
RA	SEQUENCE OF 2-99 FROM N.A.
RP	Inoue K., Kawabe Y., Kodama T.;
RL	Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases. [1]
CC	-1- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC	-1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC	-1- SIMILARITY: belongs to the TGF-beta family.
CC	-1- SIMILARITY: belongs to the TGF-beta family.
DR	EMBL; AF000133; AAB53806.1; -.
DR	HSSB; AB020217; BAA36950.1; -.
DR	HSSB; P01137; IKLA.
DR	GO: GO:0008083; F.growth factor activity; IEA.
DR	GO: GO:0008283; P.cell proliferation; IEA.
DR	GO: GO:000074; P.regulation of cell cycle; IEA.
DR	InterPro: IPR002400; GF_cyknot.
DR	InterPro: IPR001839; TGFb.
DR	Pfam: PF00019; TGF_beta; 1.
DR	PRINTS; PRO0438; GFCYSKNOT.
DR	ProDom; PD000357; TGFb; 1.
DR	SMART; SM00204; TGFB; 1.
DR	PROSITE; PS00250; TGF_BETA_1; 1.
KW	Glycoprotein; Growth Factor; Mitogen.
FT	NON_TER
FT	CHAIN
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	CONFLICT
FT	CONFLICT
TRANSFORMING GROWTH FACTOR BETA 1.	
BY SIMILARITY.	
BY SIMILARITY.	
BY SIMILARITY.	
INTERCHAIN (BY SIMILARITY).	
ID -> RS (IN REF. 2).	
PLPITYS -> AVAHNVTL (IN REF. 2).	

SO SEQUENCE 112 AA; 12795 MW; 53CSBYD46355A6F3 CRC64;

Query Match 100.0%; Score 89; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCLGPCPYWMSLDT 14
| | | | | | | | | | | | | | | | | |
Db 43 FCLGPCPYWMSLDT 56

RESULT 5

Q95N80 PRELIMINARY; PRT; 124 AA.

AC Q95N80;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE Transforming growth factor beta 1 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Fontana S., Groene A., Baumgaertner W.,
RL Submitted (FEb-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AF349538; AAK54072.1; -.
DR HSSP; P01137; 1KLA.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF beta; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor.
FT NON_TER 1 1
FT NON_TER 124 124
SQ SEQUENCE 124 AA; 14329 MW; 21D185218E556DB CRC64;

Query Match 100.0%; Score 89; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCLGPCPYWMSLDT 14
| | | | | | | | | | | | | | | | | |
Db 58 FCLGPCPYWMSLDT 71

RESULT 6

Q08714 PRELIMINARY; PRT; 130 AA.

AC Q08714; Q70331;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Transforming growth factor beta 1 (TGF-beta 1) (Fragment).
GN Name=TGFb1;
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lvg (SYR);
RX MEDLINE=93304479; PubMed=8317544;
RA Wong D.T., Donoff R.B., Yang J., Song B.Z., Matrosian K., Nagura N.,
RT Elovic A., McBride J., Gallagher G., Todd R.;
RL "Sequential expression of transforming growth factors alpha and beta 1
by eosinophils during cutaneous wound healing in the hamster.";
Am. J. Pathol. 143:130-142(1993).

RN [2]
SEQUENCE OF 26-115 FROM N.A.

RP STRAIN=SYRIAN; TISSUE=SPLEN;
RC MEDLINE=98234044; PubMed=9573100;
RX Weibly P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
RT analysis of cytokine mRNA expression in experimental visceral
RT leishmaniasis";
RL Infect. Immun. 66:2135-2142(1998).

-1- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.

-1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.

-1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.

DR EMBL; X60296; CAA42838.1; -.
DR PIR; I48196; I48196.

DR HSSP; P01137; 1KLA.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR GO; GO:0008283; P: cell proliferation; IEA.
DR GO; GO:000074; P: regulation of cell cycle; IEA.

DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF beta; 1.
DR ProDom; PD000357; TGFb; 1.

DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.

KW Glycoprotein; Growth factor; Mitogen.
FT NON_TER 1 1

FT PRODEP <1 18 TRANSFORMING GROWTH FACTOR BETA 1.
FT CHAIN 19 130 BY SIMILARITY.
FT DISULFID 25 34 BY SIMILARITY.
FT DISULFID 33 96 BY SIMILARITY.
FT DISULFID 66 129 BY SIMILARITY.
FT DISULFID 95 95 INTERCHAIN (BY SIMILARITY).
FT CONFLICT 93 93 G -> S (IN REF. 2).

SQ SEQUENCE 130 AA; 14997 MW; 8B41DD6C39C9CA77 CRC64;
Query Match 100.0%; Score 89; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCLGPCPYWMSLDT 14
| | | | | | | | | | | | | | | | | |
Db 61 FCLGPCPYWMSLDT 74

RESULT 7

TGFL_BOVIN STANDARD; PRT; 315 AA.

AC P18341;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1) (Fragment).
GN Name=TGFb1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovine; Bos.

OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=91042552; PubMed=3153459;
RA van Obberghen-Schilling E., Kondaiiah P., Ludwig R.L., Sporn M.B.,
RX Baker C.C.;
RT "Complementary deoxyribonucleic acid cloning of bovine transforming
RT growth factor-beta 1.";
RL Mol. Endocrinol. 1:693-698(1987).

RN [2]
SUBUNITS.

RC TISSUE=Bone; PubMed=1733936;
 RA MEDLINE=92129307; Daech J.R., Chang R.J., Glaser C.B.;
 RT "Purification and characterization of transforming growth factor-beta
 2.3 and -beta 1.2 heterodimers from bovine bone.";
 RL J. Biol. Chem. 267:2325-2328 (1992).
 CC -1- FUNCTION: TGF-beta is a multifunctional peptide that control
 proliferation, differentiation, and other functions in many cell
 types. Many cells synthesize TGF-beta and essentially all of them
 have specific receptors for this peptide. TGF-beta regulates the
 actions of many other peptide growth factors and determines a
 positive or negative direction of their effects. Play an important
 role in bone remodeling. It is a potent stimulator of
 osteoblastic bone formation, causing chemotaxis, proliferation and
 differentiation in committed osteoblasts (By similarity).
 CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
 covalently linked to a latency-associated peptide (LAP) homodimer.
 The inactive complex can contain a latent TGF-beta binding protein
 (By similarity). The active form is a homodimer of mature TGF-beta
 1; disulfide-linked. Heterodimers of TGF-beta 1/2 have been found
 in bone.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PFM: Glycosylated. The precursor is cleaved into mature TGF-beta 1
 and LAP (By similarity).
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M36271; AAA30778.1; -.
 DR PIR: A40057; A40057.
 DR HSSP: P01137; IKLA.
 DR InterPro: IPR002400; GF_cysknoc.
 DR InterPro: IPR003911; TGF_TGFB.
 DR InterPro: IPR001839; TGFB.
 DR InterPro: IPR001111; TGFB_N.
 DR Pfam: PF00019; TGF_beta_1.
 DR Pfam: PF00688; TGFB_propeptide; 1.
 DR PRINTS: PR00438; GFCYSKNOC.
 DR PRINTS: PR01423; TGFBETA.
 DR PRODOM: PD000357; TGFB; 1.
 DR SMART: SM00204; TGFB; 1.
 DR PROSITE: PS00250; TGF_beta_1; 1.
 DR PROSITE: PS00250; TGF_beta_1; 1.
 KW Glycoprotein; Growth factor; Mitogen.
 KM
 FT NON_TER 1
 FT PROPEP 1
 FT CHAIN 204 315 Transforming growth factor beta 1.
 FT DISULFID 210 219 By similarity.
 FT DISULFID 218 281 By similarity.
 FT DISULFID 247 312 By similarity.
 FT DISULFID 251 314 By similarity.
 FT DISULFID 280 280 Interchain (By similarity).
 FT CARBOHYD 7 7 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 61 61 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 101 101 N-linked (GlcNAc...) (By similarity).
 FT SITE 169 171 Cell attachment site (Potential).
 SQ SEQUENCE 315 AA; 36269 MW; C2717A23D94E00E CRC64;
 Query Match 100.0%; Score 89; DB 1; Length 315;
 Best Local Similarity 100.0%; Pred. No. 8.8e-06; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0;
 QY 1 FCLGPCPYIWSLDT 14
 DB 246 FCLGPCPYIWSLDT 259

Q8R4D9
 ID Q8R4D9 PRELIMINARY; PRT; 368 AA.
 AC Q8R4D9
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Transforming growth factor beta-1 protein (Fragment).
 GN Name=Tgfb1;
 OS Sigmoidon hispidus (Hispid cotton rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 CC Sigmodon.
 OX NCBI_TaxID=42415;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=14980081; DOI=10.1089/10799900477219873;
 RA Blanco J.C., Plateney L., Boukhalova M., Richardson J.Y.,
 Harris K.A., Prince G.A.;
 RT "The cotton rat: an underutilized animal model for human infectious
 diseases can now be exploited using specific reagents to cytokines,
 chemokines, and interferons.";
 RT J. Interferon Cytokine Res. 24:21-28 (2004).
 RL -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PFM: Glycosylated. The precursor is cleaved into mature TGF-beta 1
 and LAP (By similarity).
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF480858; AA87199.1; -.
 DR HSSP: P01137; IKLA.
 DR GO: GO:0008083; F:growth factor activity; IEA.
 DR GO: GO:0005160; F:transforming growth factor beta receptor bi.; IEA.
 DR GO: GO:0016049; F:cell growth; IEA.
 DR InterPro: IPR002400; GF_cysknoc.
 DR InterPro: IPR001839; TGFB.
 DR InterPro: IPR001111; TGFB_N.
 DR InterPro: IPR003911; TGF_TGFB.
 DR Pfam: PF00688; TGFB_propeptide; 1.
 DR Pfam: PF00019; TGF_beta_1.
 DR PRINTS: PR00438; GFCYSKNOC.
 DR PRINTS: PR01423; TGFBETA.
 DR PRODOM: PD000357; TGFB; 1.
 DR SMART: SM00204; TGFB; 1.
 DR PROSITE: PS00250; TGF_beta_1; 1.
 KM Growth factor.
 FT NON_TER 1
 FT SEQUENCE 368 AA; 41905 MW; A5C91207B0468B4A CRC64;
 Query Match 100.0%; Score 89; DB 2; Length 368;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FCLGPCPYIWSLDT 14
 DB 299 FCLGPCPYIWSLDT 312

RESULT 9
 ID TGF1_CANFA STANDARD; PRT; 390 AA.
 AC P54831;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).
 GN Name=TGFb1;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Jugular vein endothelial;
 RX MEDLINE=95237630; PubMed=7721110; DOI=10.1016/0378-1119(94)00903-6;
 RA Manning A.W., Auchampach J.A., Drong R.F., Slightom J.L.;
 RT "Cloning of a canine CDNA homologous to the human transforming growth

RT factor-beta 1-encoding gene.";
 RL Gene 155:307-308(1995).
 CC -1- FUNCTION: TGF-beta is a multifunctional peptide that control
 CC proliferation, differentiation, and other functions in many cell
 CC types. Many cells synthesize TGF-beta and essentially all of them
 CC have specific receptors for this peptide. TGF-beta regulates the
 CC actions of many other peptide growth factors and determines a
 CC positive or negative direction of their effects. Play an important
 CC role in bone remodeling. It is a potent stimulator of
 CC osteoblastic bone formation, causing chemotaxis, proliferation and
 CC differentiation in committed osteoblasts (By similarity).
 CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
 CC covalently linked to a latency-associated peptide (LAP) homodimer.
 CC The inactive complex can contain a latent TGF-beta binding
 CC protein. The active form is a homodimer of mature TGF-beta 1;
 CC disulfide-linked (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1
 CC and LAP (By similarity).
 CC -1- SIMILARITY: Belongs to the TGF-beta family.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

 DR EMBL: L34956; AAA51458.1; -.
 DR PIR: JC4023; JC4023.
 DR HSSP: P01137; IKLA.
 DR InterPro: IPR002400; GF_cyskn0t.
 DR InterPro: IPR003911; TGF_TGFB.
 DR InterPro: IPR001839; TGFb.
 DR InterPro: IPR01111; TGFb_N.
 DR Pfam: PF00019; TGF_beta; 1.
 DR Pfam: PF00688; TGFb_propeptide; 1.
 DR PRINTS: PR00438; GRCYSKN0T.
 DR PRINTS: PR01423; TGFbBETA.
 DR PRODOM: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 KM Glycoprotein; Growth Factor; Mitogen; Signal.
 FT SIGNAL 1 29
 FT PROPEP 30 28
 FT CHAIN 279 390
 FT DISULFID 285 294
 FT DISULFID 293 356
 FT DISULFID 322 387
 FT DISULFID 326 389
 FT DISULFID 355 355
 FT CARBOHYD 82 82
 FT CARBOHYD 136 136
 FT CARBOHYD 176 176
 FT SITE 244 246
 SQ SEQUENCE 390 AA; 44185 MW; E84780E88B7B590E CRC64;
 Query Match 100.0%; Score 89; DB 1; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1;le-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 16-OCT-2001 (Rel. 40, last sequence update)
 DT 05-JUL-2004 (Rel. 44, last annotation update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).
 GN Name=TGFb1;
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OK NCBI_Taxid=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Hartley;
 RA Jeevan A.; McMurray D.N.; Yoshimura T.;
 RT "Guinea pig transforming growth factor-beta in peritoneal exudates
 RT after BCG vaccination.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 265-382 FROM N.A.
 RX MEDLINE=99144670; PubMed=10025978; DOI=10.1016/S1043-4666(98)90002-3;
 RA Scarozza A.M.; Ramsingh A.I.; Wicher V.; Wicher K.;
 RT "Spontaneous cytokine gene expression in normal guinea pig blood and
 RT tissues".
 RL Cytokine 10:851-859(1998).
 RN [3]
 RP SEQUENCE OF 279-371 FROM N.A.
 RC STRAIN=Hartley; TISSUE=Trachea;
 RA Morishima Y.; Uchida Y.; Nomura A.; Ishii Y.; Sakamoto T.;
 RA Seizawa K.;
 RT "Guinea-pig transforming growth factor-beta expression in injured
 RT tracheal epithelium.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Multifunctional peptide that controls proliferation,
 CC differentiation, and other functions in many cell types. Many
 CC cells synthesize TGF-beta 1 and essentially all of them have
 CC specific receptors for this peptide. TGF-beta 1 regulates the
 CC actions of many other peptide growth factors and determines a
 CC positive or negative direction of their effects. Play an important
 CC role in bone remodeling. It is a potent stimulator of
 CC osteoblastic bone formation, causing chemotaxis, proliferation and
 CC differentiation in committed osteoblasts (By similarity).
 CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
 CC covalently linked to a latency-associated peptide (LAP) homodimer.
 CC The inactive complex can contain a latent TGF-beta binding
 CC protein. The active form is a homodimer of mature TGF-beta 1;
 CC disulfide-linked (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1
 CC and LAP (By similarity).
 CC -1- SIMILARITY: Belongs to the TGF-beta family.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

 DR EMBL: AF191297; AF02780.1; -.
 DR EMBL: AF097509; AAC83807.1; -.
 DR EMBL: AF169347; AAD49347.1; -.
 DR HSSP: P01137; IKLA.
 DR InterPro: IPR002400; GF_cyskn0t.
 DR InterPro: IPR003911; TGF_TGFB.
 DR InterPro: IPR001839; TGFb.
 DR InterPro: IPR01111; TGFb_N.
 DR Pfam: PF00019; TGF_beta; 1.
 DR Pfam: PF00688; TGFb_propeptide; 1.
 DR PRINTS: PR00438; GRCYSKN0T.
 DR PRINTS: PR01423; TGFbBETA.
 DR PRODOM: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 KM Glycoprotein; Growth Factor; Mitogen; Signal.

```

FT SIGNAL 1 29 By similarity.
FT PROPEP 30 278 latency-associated peptide (By
FT CHAIN 279 390 similarity).
FT DISULFID 285 294 Transforming growth factor beta 1.
FT DISULFID 293 356 By similarity.
FT DISULFID 322 387 By similarity.
FT DISULFID 326 389 By similarity.
FT CARBOHYD 355 355 Interchain (By similarity).
FT CARBOHYD 82 82 N-linked (GlcNAc... ) (By similarity).
FT CARBOHYD 136 136 N-linked (GlcNAc... ) (By similarity).
FT CARBOHYD 176 176 Cell attachment site (Potential).
FT SITE 244 246 G -> P (in Ref. 3).
FT CONFLICT 279 279 F -> S (in Ref. 2).
FT CONFLICT 286 286 K -> E (in Ref. 2).
FT CONFLICT 309 309 C -> R (in Ref. 2).
FT CONFLICT 322 322 A -> G (in Ref. 2).
FT CONFLICT 350 350
SQ SEQUENCE 390 AA; 44328 MW; 1539F849BA0C0CF1 CRC64;

Query Match 100.0%; Score 89; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCILGPCYIWSLDT 14
Db 321 FCILGPCYIWSLDT 334

RESULT 11
TGFL_HORSE STANDARD; PRT; 390 AA.
ID _TGFL_HORSE
AC P09533;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN Name=TGFb1;
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=67246074; PubMed=3474130;
RA Sharples K., Plowman G.D., Rose T.M., Twardzik D.R., Purchio A.F.;
RT "Cloning and sequence analysis of simian transforming growth factor-
beta cDNA."
RL DNA 6:235-244(1987).
RN [2]
RX GLYCOSYLATION.
RX PubMed=2971654;
RA Purchio A.F., Cooper J.A., Brunner A.M., Lioubin M.N., Gentry L.E.,
RA Kovachina K.S., Roth R.A., Marguardt H.;
RT "Identification of mannose 6-phosphate in two asparagine-linked sugar
chains of recombinant transforming growth factor-beta 1 precursor."
RL J. Biol. Chem. 263:14211-14215(1988).
RN [3]
RX CHARACTERIZATION.
RX PubMed=3185545;
RA Gentry L.E., Lioubin M.N., Purchio A.F., Marguardt H.;
RT "Molecular events in the processing of recombinant type 1 pre-pro-
transforming growth factor beta to the mature polypeptide."
RL Mol. Cell. Biol. 8:4162-4168(1988).
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN Name=TGFb1;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RX SEQUENCE FROM N.A.

```

```

CC differentiation in committed osteoblasts (By similarity).
CC -1 SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
CC covalently linked to a latency-associated peptide (LAP) homodimer.
CC The inactive complex can contain a latent TGF-beta binding
CC protein. The active form is a homodimer of mature TGF-beta 1;
CC disulfide-linked.
CC -1 SUBCELLULAR LOCATION: Secreted.
CC -1 PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1
CC and LAP, which remains non-covalently linked to mature TGF-beta 1
CC rendering it inactive.
CC -1 SIMILARITY: Belongs to the TGF-beta family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.1db-61b.ch/announce/
CC or send an email to license@1db-61b.ch).
CC -----
CC EMBL; M16658; AAA35369.1; -.
CC PIR; A26960; A26960.
CC HSSP; P01137; IRLA.
CC InterPro; IPR002400; GF_cysknot.
CC InterPro; IPR003911; TGF_TGFB.
CC InterPro; IPR001839; TGFB.
CC InterPro; IPR001111; TGFB_N.
CC Pfam; PF00019; TGFB_beta; 1.
CC Pfam; PF00688; TGFB_propeptide; 1.
CC PRINTS; PR00438; GRCYSKNOT.
CC PRINTS; PR01423; TGFBR1.
CC PRODOM; PD000357; TGFB; 1.
CC SMART; SM00204; TGFB; 1.
CC PROSITE; PS00250; TGF_BETA_1; 1.
CC Glycoprotein; Growth Factor; Mitogen; Signal.
CC SIGNAL 1 29
CC PROPEP 30 278 latency-associated peptide.
CC CHAIN 279 390 Transforming growth factor beta 1.
CC DISULFID 285 294 By similarity.
CC DISULFID 293 356 By similarity.
CC DISULFID 322 387 By similarity.
CC DISULFID 326 389 By similarity.
CC CARBOHYD 355 355 Interchain (By similarity).
CC CARBOHYD 82 82 N-linked (GlcNAc... ) (By similarity).
CC CARBOHYD 136 136 N-linked (GlcNAc... ) (By similarity).
CC CARBOHYD 176 176 N-linked (GlcNAc... ) (By similarity).
CC SITE 244 246 Cell attachment site (Potential).
SQ SEQUENCE 390 AA; 44356 MW; DFF63E2BAB46320B CRC64;

Query Match 100.0%; Score 89; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCILGPCYIWSLDT 14
Db 321 FCILGPCYIWSLDT 334

RESULT 12
TGFL_HORSE STANDARD; PRT; 390 AA.
ID _TGFL_HORSE
AC O19011;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN Name=TGFb1;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RX SEQUENCE FROM N.A.

```

CC TISSUE=Lymph node;
 RX MEDLINE=98185507; PubMed=9524819;
 RA Penha-Goncalves M.N., Onions D.E., Nicolson L.;
 RT "Cloning and sequencing of equine transforming growth factor-beta 1
 (TGF-beta-1) cDNA."
 RL DNA Seq. 7:375-378(1997).
 CC -1 FUNCTION: TGF-beta is a multifunctional peptide that control
 proliferation, differentiation, and other functions in many cell
 types. Many cells synthesize TGF-beta and essentially all of them
 have specific receptors for this peptide. TGF-beta regulates the
 actions of many other peptide growth factors and determines
 positive or negative direction of their effects. Play an important
 role in bone remodelling. It is a potent stimulator of
 osteoblastic bone formation, causing chemotaxis, proliferation and
 differentiation in committed osteoblasts (by similarity).
 CC -1 SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
 covalently linked to a latency-associated peptide (LAP) homodimer.
 CC The inactive complex can contain a latent TGF-beta binding
 protein. The active form is a homodimer of mature TGF-beta 1;
 CC disulfide-linked (by similarity).
 CC -1 SUBCELLULAR LOCATION: Secreted.
 CC -1 PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1
 and LAP (by similarity).
 CC -1 SIMILARITY: Belongs to the TGF-beta family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).
 CC -----

DR EMBL; X99438; CA67801.1; -.
 DR HSPB; P01137; 1KLA.
 DR InterPro: IPR002400; GF_cysknoc.
 DR InterPro: IPR003911; TGF_TGFB.
 DR InterPro: IPR001839; TGFb.
 DR InterPro: IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF_beta_1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PR00438; GFCYSKNOC.
 DR PRINTS; PR01423; TGFbeta.
 DR PRODOM; PD000357; TGFb_1.
 DR SMART; SM00204; TGFb_1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KM Glycoprotein; Growth factor; Mitogen; Signal.
 FT SIGNAL 1 29
 FT PROPEP 30 278
 FT CHAIN 279 390
 FT DISULFID 285 294
 FT DISULFID 293 356
 FT DISULFID 322 387
 FT DISULFID 326 389
 FT DISULFID 355 355
 FT CARBOHYD 82 82
 FT CARBOHYD 136 136
 FT CARBOHYD 176 176
 SO SEQUENCE 390 AA; 43974 MW; A86D715F44549691 CRC64;

Query Match 100.0%; Score 89; DB 1; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FCLGCPYMSLDT 14
 |||||
 DB 321 FCLGCPYMSLDT 334

RESULT 13
 TGF1_HUMAN
 ID TGF1_HUMAN STANDARD; PRT; 390 AA.

AC P01137; Q9UCG4;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).
 GN Name=TGFb1; Synonyms=TGFb;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87174845; PubMed=3470709;
 RA Derynck R., Rhee L., Chen E.Y., van Tilburg A.;
 RT "Intron-exon structure of the human transforming growth factor-beta
 precursor gene."
 RL Nucleic Acids Res. 15:3188-3189(1987).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANT PRO-10.
 RX MEDLINE=85296301; PubMed=3861940;
 RA Derynck R., Jarrett J.A., Chen E.Y., Eaton D.H., Bell J.R.,
 RA Assoian R.K., Roberts A.B., Sporn M.B., Goeddel D.V.;
 RT "Human transforming growth factor-beta complementary DNA sequence and
 expression in normal and transformed cells."
 RL Nature 316:701-705(1985).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Dundenum, and Eye;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Streusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.J., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Alechuk S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshimiyki S., Carrincci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wortley K.C., Hale S., Garcia A.M., Gay L.J., Halyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska V., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [4]
 RN SEQUENCE OF 279-390 FROM N.A.
 RP TISSUE=Cardioma;
 RA Urushizaki Y., Tereu T., Koshida Y., Mahara K., Kohgo Y.,
 RA Urushizaki I., Takahashi Y., Ito H.;
 RT "Cloning and expression of the gene for human transforming growth
 factor-beta in *Escherichia coli*."
 RL Tumor Res. 22:41-55(1987).
 RN [5]
 RP SEQUENCE OF 279-329.
 RC TISSUE=Bladder carcinoma;
 RX MEDLINE=93229900; PubMed=8471846; DOI=10.1006/prep.1993.1019;
 RA Bourdrel L., Lin C.-H., Lauren S.L., Elmore R.H., Sugerman B.J.,
 RA Hu S., Westcott K.R.;
 RT "Recombinant human transforming growth factor-beta 1: expression by
 Chinese hamster ovary cells, isolation, and characterization."
 RL Protein Expr. Purif. 4:130-140(1993).
 RN [6]
 RP SEQUENCE OF 279-301.
 RX MEDLINE=85131019; PubMed=2982829;
 RA Masague J., Like B.;
 RT "Cellular receptors for type beta transforming growth factor. Ligand
 binding and affinity labeling in human and rodent cell lines."
 RL J. Biol. Chem. 260:2636-2645(1985).

[7]
RP SEQUENCE OF 30-42 AND 279-290. AND CHARACTERIZATION.
RX PubMed=3162913;
RA Miyazono K., Hellman U., Wernstedt C., Heldin C.H.;
RT "Latent high molecular weight complex of transforming growth factor
beta 1. Purification from human platelets and structural
characterization.";
RL J. Biol. Chem. 263:6407-6415 (1988).
RN [8]
RP REVIEW.
RX PubMed=9150447;
RA Minger J.S., Hapel J.G., Gleizes P.E., Mazzieri R., Nunes I.,
RA Rifkin D.B.;
RT "Latent transforming growth factor-beta: structural features and
mechanisms of activation.";
RL Kidney Int. 51:1376-1382 (1997).
RN [9]
RP STRUCTURE BY NMR OF 279-390.
RX MEDLINE=93144313; PubMed=8424942;
RA Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez K.A.,
RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
RA Torchia D.A.;
RT "Transforming growth factor beta 1: NMR signal assignments of the
recombinant protein expressed and isotopically enriched using Chinese
hamster ovary cells.";
RL Biochemistry 32:1152-1163 (1993).
RN [10]
RP STRUCTURE BY NMR OF 279-390.
RX MEDLINE=93144320; PubMed=8424943;
RA Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez K.A.,
RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
RA Torchia D.A.;
RT "Transforming growth factor beta 1: secondary structure as determined
by heteronuclear magnetic resonance spectroscopy.";
RL Biochemistry 32:1164-1171 (1993).
RN [11]
RP STRUCTURE BY NMR OF 279-390.
RX MEDLINE=96266150; PubMed=8679613; DOI=10.1021/bi9604946;
RA Hinck A.P., Archer S.J., Qian S.W., Roberts A.B., Sporn M.B.,
RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
RA Torchia D.A.;
RT "Transforming growth factor beta 1: three-dimensional structure in
solution and comparison with the X-ray structure of transforming
growth factor beta 2.";
RL Biochemistry 35:8517-8534 (1996).
RN [12]
RP TISSUE SPECIFICITY.
RX PubMed=11746498; DOI=10.1002/jcb.1249;
RA Shur I., Lokiec F., Bleiberg I., Benayahu D.;
RT "Differential gene expression of cultured human osteoblasts.";
RL J. Cell. Biochem. 83:547-553 (2001).
RN [13]
RP VARIANT PRO-10.
RX PubMed=9783545;
RA Yamada Y., Miyauchi A., Goto J., Takagi Y., Okizumi H., Kanematsu M.,
RA Hase M., Takai H., Harada A., Ikeda K.;
RT "Association of a polymorphism of the transforming growth factor-beta1
gene with genetic susceptibility to osteoporosis in postmenopausal
Japanese women.";
RL J. Bone Miner. Res. 13:1569-1576 (1998).
RN [14]
RP VARIANTS CED CYS-218, HIS-218 AND ARG-225.
RX PubMed=10973241; DOI=10.1038/79128;
RA Kinoshita A., Saito T., Tomita H., Makita Y., Yoshida K., Ghadami M.,
RA Yamada K., Kondo S., Ikegawa S., Nishimura G., Fukushima Y.,
RA Nakagomi T., Saito H., Sugimoto T., Kamegaya M., Hise K., Murray J.C.,
RA Taniguchi N., Nishikawa N., Yoshimura K.;
RT "Domain-specific mutations in TGFBI result in Camurati-Engelmann
disease.";
RL Nat. Genet. 26:19-20 (2000).
RN [15]
RP VARIANTS CED HIS-81, CYS-218 AND ARG-225.
RX PubMed=11062463; DOI=10.1038/81563;

RA Janssens K., Gershoni-Baruch R., Guanabens N., Migone N., Ralston S.,
RA Bonduelle M., Lissens W., Van Maldergem L., Vanhoenacker F.,
RA Verbruggen L., Van Hul W.;
RT "Mutations in the gene encoding the latency-associated peptide of TGF-
beta 1 cause Camurati-Engelmann disease.";
RL Nat. Genet. 26:273-275 (2000).
RN [16]
RP VARIANT PRO-10.
RX PubMed=12202987; DOI=10.1007/s100380200069;
RA Watanabe Y., Kinoshita A., Yamada T., Ohta T., Kishino T.,
RA Matsumoto N., Ishikawa M., Nishikawa N., Nishimura K.;
RT "A catalog of 106 single-nucleotide polymorphisms (SNPs) and 11 other
types of variations in genes for transforming growth factor-beta1
(TGF-beta1) and its signaling pathway.";
RL J. Hum. Genet. 47:478-483 (2002).
RN [17]
RP CHARACTERIZATION OF VARIANTS CED HIS-81, CYS-218, ASP-222 AND ARG-225.
RX PubMed=12493741; DOI=10.1074/jbc.M208857200;
RA Janssens K., ten Dijke P., Ralston S.H., Bergmann C., Van Hul W.;
RT "Transforming growth factor-beta-1 mutations in Camurati-Engelmann
disease lead to increased signaling by altering either activation or
secretion of the mutant protein.";
RL J. Biol. Chem. 278:7718-7724 (2003).
RN [18]
RP CHARACTERIZATION OF VARIANT CYS-218.
RX PubMed=12843182; DOI=10.1210/jc.2002-020564;
RA McGowan N.W., Macpherson H., Janssens K., Van Hul W., Fitch J.C.,
RA Fraser W.D., Ralston S.H., Helfrich M.H.;
RT "A mutation affecting the latency-associated peptide of TGFbeta1 in
Camurati-Engelmann disease enhances osteoclast formation in vitro.";
RL J. Clin. Endocrinol. Metab. 88:3321-3326 (2003).
RN [19]
RP FUNCTION: Multifunctional peptide that controls proliferation,
differentiation, and other functions in many cell types. Many
cells synthesize TGF-beta 1 and essentially all of them have
specific receptors for this peptide. TGF-beta 1 regulates the
actions of many other peptide growth factors and determines a
positive or negative direction of their effects. Play an important
role in bone remodeling. It is a potent stimulator of
osteoblastic bone formation, causing chemotaxis, proliferation and
differentiation in committed osteoblasts (By similarity).
CC -I SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
covalently linked to a latency-associated peptide (LAP) homodimer.
CC The inactive complex can contain a latent TGF-beta binding
protein. The active form is a homodimer of mature TGF-beta 1;
CC disulfide-linked.
CC -I SUBCELLULAR LOCATION: Secreted.
CC -I TISSUE SPECIFICITY: Highly expressed in bone.
CC -I INDUCTION: Activated in vitro at pH below 3.5 and over 12.5.
CC -I PTM: Glycosylated (By similarity). The precursor is cleaved into
CC mature TGF-beta 1 and LAP.
CC -I POLYMORPHISM: In post-menopausal Japanese women, the frequency of
CC Leu-10 is higher in subjects with osteoporosis than in controls.
CC -I DISEASE: Defects in TGFBI are the cause of Camurati-Engelmann
Query Match 100.0%; Score 89; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 1,1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 FCLGCPYIWSLDT 14
Db 321 FCLGCPYIWSLDT 334
RESULT 14
TGF1 MOUSE
ID TGF1 MOUSE STANDARD; PRT; 390 AA.
AC P04202;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN Name=tgfb1;
OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 CC [1]
 CC SEQUENCE FROM N.A.
 RX MEDLINE=86168129; PubMed=3007454;
 RA Derynck R., Jarrett J.A., Chen B.Y., Goeddel D.V.,
 RT "The murine transforming growth factor-beta precursor.";
 RL J. Biol. Chem. 261:4377-4379(1986).
 CC [2]
 CC SEQUENCE FROM N.A.
 RP STRAIN=BAB/c;
 RX MEDLINE=96096545; PubMed=8522200; DOI=10.1016/0378-1119(95)00460-N;
 RA Guron C., Sudarshan C., Raghov R.,
 RT "Molecular organization of the gene encoding murine transforming
 RT growth factor beta 1.";
 RL Gene 165:325-326(1995).
 CC [3]
 CC SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6, and NOD/Lt; TISSUE=Spleen;
 RA Poitrot L., Benoist C., Mathis D.,
 RT "Transforming growth factor-beta 1 sequence and expression: no
 RT difference between NOD/Lt and C57BL/6 mouse strains.";
 RL Submitted (Aug-1998) to the EMBL/Genbank/DBJ databases.
 CC [4]
 CC SEQUENCE FROM N.A.
 RP STRAIN=FVB/N; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stajich T.L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinot P., Frange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: TGF-beta is a multifunctional peptide that control
 CC proliferation, differentiation, and other functions in many cell
 CC types. Many cells synthesize TGF-beta and essentially all of them
 CC have specific receptors for this peptide. TGF-beta regulates the
 CC actions of many other peptide growth factors and determines a
 CC positive or negative direction of their effects. Play an important
 CC role in bone remodelling. It is a potent stimulator of
 CC osteoblastic bone formation, causing chemotaxis, proliferation and
 CC differentiation in committed osteoblasts (By similarity).
 CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
 CC covalently linked to a latency-associated peptide (LAP) homodimer.
 CC The inactive complex can contain a latent TGF-beta binding
 CC protein. The active form is a homodimer of mature TGF-beta 1;
 CC disulfide-linked (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1
 CC and LAP (By similarity).
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

CC or send an email to license@isb-sib.ch.
 CC -----
 CC EMBL; M13177; AAA40423.1; -;
 CC EMBL; L42462; AAB00138.1; -;
 CC EMBL; L42456; AAB00138.1; JOINED.
 CC EMBL; L42457; AAB00138.1; JOINED.
 CC EMBL; L42458; AAB00138.1; JOINED.
 CC EMBL; L42459; AAB00138.1; JOINED.
 CC EMBL; L42460; AAB00138.1; JOINED.
 CC EMBL; L42461; AAB00138.1; JOINED.
 CC EMBL; A009862; CAA08900.1; -;
 CC EMBL; BC013738; AAH13738.1; -;
 CC PIR; A01396; WFMS2.
 CC HSSP; P01137; IKLA.
 CC MGD; MGI:98725; Tgfb1.
 CC GO; GO:0005578; C:extracellular matrix; IDA.
 CC GO; GO:0006954; P:inflammatory response; IMP.
 CC GO; GO:0007515; P:lymph gland development; IMP.
 CC GO; GO:0006820; P:necrosis; IMP.
 CC GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
 CC GO; GO:0042127; P:regulation of cell proliferation; IDA.
 CC GO; GO:0042306; P:regulation of myogenesis; IDA.
 CC GO; GO:007179; P:transforming growth factor beta receptor si. .; IDA.
 CC InterPro; IPR002400; GF_cytknot.
 CC InterPro; IPR003911; TGF_TGFB.
 CC InterPro; IPR001839; TGFB.
 CC InterPro; IPR001111; TGFB_N.
 CC Pfam; PF00019; TGF_beta_1.
 CC Pfam; PF00688; TGFB_propeptide; 1.
 CC PRINTS; PR00438; GFCYSNOT.
 CC PRINTS; PR01423; TGFBETA.
 CC ProDom; PD000357; TGFB_1.
 CC PROSITE; PS00250; TGF_BETA_1; 1.
 CC KAM; Glycoprotein; Growth factor; Mitogen; Signal.
 CC FT SIGNAL 1 29
 CC FT PROPEP 30 278
 CC FT CHAIN 279 390
 CC FT DISULFD 285 294
 CC FT DISULFD 293 356
 CC FT DISULFD 322 387
 CC FT DISULFD 326 389
 CC FT DISULFD 355 355
 CC FT CARBOHYD 82 82
 CC FT CARBOHYD 136 136
 CC FT CARBOHYD 176 176
 CC FT SITE 244 246
 CC SQ SEQUENCE 390 AA; 44310 MW; 4381A51B711D689E CRC64;
 CC
 CC Query Match 100.0%; Score 89; DB 1; Length 390;
 CC Best Local Similarity 100.0%; Pred. NO. 1.1e-05;
 CC Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 FCLGPCPYIWSLDT 14
 CC DB 321 FCLGPCPYIWSLDT 334
 CC
 CC RESULT 15
 CC ID TGF1_PIG STANDARD; PRT; 390 AA.
 CC AC P07200; P08832;
 CC DT 01-APR-1988 (Rel. 07, Created)
 CC DT 01-APR-1988 (Rel. 07, Last sequence update)
 CC DT 05-JUN-2004 (Rel. 44, Last annotation update)
 CC DE Transforming growth factor beta 1 precursor (TGF-beta 1).
 CC GN Name=TGFBI;
 CC OS Sus scrofa (Pig).
 CC CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 CC OX NCBI_TaxID=9823;
 CC RN [1]
 CC SEQUENCE FROM N.A.

RC TISSUE=Ovary;
RX MEDLINE=87174844; PubMed=3470708;
RA Derynck R., Rhee L.;
RT "Sequence of the porcine transforming growth factor-beta precursor";
RL Nucleic Acids Res. 15:3187-3187(1987).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT VAL-114.
RC STRAIN=miniature swine;
RX MEDLINE=89054010; PubMed=2461367;
RA Kondalish P., van Obberghen-Schilling E., Ludwig R.L., Dhar R.,
RA Sporn M.B., Roberts A.B.;
RT "cDNA cloning of porcine transforming growth factor-beta 1 mRNAs.
RT Evidence for alternate splicing and polyadenylation.";
RL J. Biol. Chem. 263:18313-18317(1988).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT VAL-114.
RX MEDLINE=88335639; PubMed=3166520;
RA Jakowlew S.B., Dillard P.U., Sporn M.B., Roberts A.B.;
RT "Nucleotide sequence of chicken transforming growth factor-beta 1
RT (TGF-beta 1).";
RL Nucleic Acids Res. 16:8730-8730(1988).
RN [4]
RP SHOWS THAT REF.3 SEQUENCE IS FROM PTG.
RA Jakowlew S.B.;
RL Unpublished observations (MAR-1996).
RN [5]
RP SEQUENCE FROM N.A., AND VARIANT VAL-114.
RA Wimmers K., Chomdej S., Ponsuksell S., Schellander K.;
RT "Polymorphism in the porcine transforming growth factor beta 1 gene";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 279-322.
RX MEDLINE=87102890; PubMed=2879635; DOI=10.1016/0092-8674(87)90192-9;
RA Chelifetz S., Weatherbee J.A., Tsang M.L.S., Anderson J.K., Mole J.E.,
RA Lucas R., Massague J.;
RT "The transforming growth factor-beta system, a complex pattern of
RT cross-reactive ligands and receptors.";
RL Cell 48:409-415(1987).
CC -1- FUNCTION: TGF-beta is a multifunctional peptide that control
CC proliferation, differentiation, and other functions in many cell
CC types. Many cells synthesize TGF-beta and essentially all of them
CC have specific receptors for this peptide. TGF-beta regulates a
CC actions of many other peptide growth factors and determines a
CC positive or negative direction of their effects. Play an important
CC role in bone remodeling. It is a potent stimulator of
CC osteoblastic bone formation, causing chemotaxis, proliferation and
CC differentiation in committed osteoblasts (By similarity).
CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
CC covalently linked to a latency-associated peptide (LAP) homodimer.
CC The inactive complex can contain a latent TGF-beta binding
CC protein. The active form is a homodimer of mature TGF-beta 1;
CC disulfide-linked (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1
CC and LAP (By similarity).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC -1- CAUTION: Ref.3 sequence which was said to originate from chicken
CC white leghorn, seems (Ref.4) to originate from pig.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y00111; CA68291.1; -;
CC EMBL; M23703; AAA64616.1; -;
CC EMBL; X12373; CAA30933.1; -;
CC EMBL; AF461808; AAL57902.1; -;
CC F01; A27512; A27512.
CC PIR; S01413; S01413.

DR HSSP; P01137; 1KLA.
DR InterPro; IPR002400; GE_cysknot.
DR InterPro; IPR003911; TGF_TGFB.
DR InterPro; IPR001839; TGFB.
DR InterPro; IPR001111; TGFB_N.
DR Pfam; PF00019; TGF_beta; 1.
DR Pfam; PF00688; TGFB_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR01423; TGFBETA.
DR ProDom; PD000357; TGFB; 1.
DR SMART; SM00204; TGFB; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Direct protein sequencing; Glycoprotein; Growth factor; Mitogen;
KW Polymorphism; Signal.
FT SIGNAL 1 29
FT PROPEP 30 278 By similarity.
FT CHAIN 279 390 Transforming growth factor beta 1.
FT DISULFID 285 294 By similarity.
FT DISULFID 293 356 By similarity.
FT DISULFID 322 387 By similarity.
FT DISULFID 326 389 By similarity.
FT DISULFID 355 355 Interchain (By similarity).
FT CARBOHYD 82 82 N-linked (GlcNAc...) (By similarity).
FT CARBOHYD 136 136 N-linked (GlcNAc...) (By similarity).
FT CARBOHYD 176 176 N-linked (GlcNAc...) (By similarity).
FT SITE 244 246 Cell attachment site (Potential).
FT VARIANT 114 114 L -> V.
FT CONFLICT 6 7 LR -> PG (in Ref. 3).
FT CONFLICT 180 180 R -> G (in Ref. 3).
FT CONFLICT 237 237 N -> NA (in Ref. 3).
SQ SEQUENCE 390 AA; 44294 MW; A6E2C3659FC384E6 CRC64;

Query Match 100.0%; Score 89; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 1; e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FCLGPPCYIWSLDT 14
DB 321 FCLGPPCYIWSLDT 334

Search completed: June 14, 2005, 15:51:06
Job time : 74.8462 secs

XX Sequence 23 AA;

Query Match 100.0%; Score 145; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 4,3e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HEPKGYHANFCLGCPPIYMSLDT 23
DB 1 HEPKGYHANFCLGCPPIYMSLDT 23

RESULT 2
AA92954
ID AAY92954 standard; peptide; 23 AA.

XX AAY92954;

XX 08-NOV-2000 (first entry)

XX Transforming growth factor inhibitory peptide #10.

XX Hepatotropic; antagonist; transforming growth factor beta1; TGF- β 1;
XX competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX extracellular matrix degradation inhibitor; mimotope; cirrhosis.

XX Homo sapiens.

XX WO200031135-A1.

XX 02-JUN-2000.

XX 23-NOV-1999; 99WO-ES000375.

XX 24-NOV-1998; 98ES-00002465.

XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagaribelza JJ, Prieto Valtuena J;
XX Borras Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor beta1,
XX useful for treatment of liver disease, especially cirrhosis, are partial
XX sequences of the factor or its receptors.

XX Claim 11, Page 82; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding
XX of transforming growth (TGF) factor beta1 (TGF- β 1) to its receptor in
XX vivo which have partial amino acid sequences identical, or similar, with
XX those of TGF- β 1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX examples of the peptides of the invention. The peptides act by
XX competitive inhibition of the binding of TGF- β 1 to its receptors, e.g.
XX they are inhibitors of stimulation of collagen synthesis in liver cells
XX and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX extracellular matrix. The peptides, their mimotopes and/or DNA (or
XX expression systems) encoding the peptides are used for treatment of liver
XX disease, specifically cirrhosis

XX Sequence 23 AA;

Query Match 100.0%; Score 145; DB 3; Length 23;

Best Local Similarity 100.0%; Pred. No. 4,3e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HEPKGYHANFCLGCPPIYMSLDT 23
DB 1 HEPKGYHANFCLGCPPIYMSLDT 23

RESULT 3

AAR90828
ID AAR90828 standard; peptide; 50 AA.

XX AAR90828;

XX 25-MAR-2003 (revised)
XX 25-JAN-1980 (first entry)

XX Pre-transforming growth factor beta 1 residues 252 to 302.

XX transforming growth factor beta 1; wound healing; recombinant production.

XX Homo sapiens.

XX US5482851-A.

XX 09-JAN-1996.

XX 05-NOV-1993; 93US-00147364.

XX 22-MAR-1985; 85US-00715142.

XX 13-MAR-1987; 87US-00025423.

XX 04-AUG-1989; 89US-00389929.

XX 04-MAR-1992; 92US-00845893.

XX (GETH) GENENTECH INC.

XX Goeddel DV, Derynck RMA;

XX WPI; 1996-076891/08.

XX N-PSDB; AAT15721.

XX New recombinant human transforming growth factor-beta prods. - produced
XX using Chinese hamster ovary cells, for use in diagnostic applications or
XX in therapy.

XX Example 2; Fig 2; 26pp; English.

XX The transforming growth factor (TGF) beta 1 exon (residues 252 to 302)
XX was identified using the "long probe" strategy used previously for TGF-
XX alpha. Long oligonucleotides (T1572-23) designed on the basis of the
XX partial protein sequence were used as hybridisation probes for the exon
XX in a human genomic DNA library. The TGF beta 1 exon was then used as a
XX probe for the isolation of TGF beta 1 cDNA (see AAT15270). DNA encoding
XX TGF beta 1 is useful for the recombinant production of the protein, which
XX is useful in, e.g. wound healing. (Updated on 25-MAR-2003 to correct PF
XX field.)

XX Sequence 50 AA;

Query Match 100.0%; Score 145; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 8,7e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HEPKGYHANFCLGCPPIYMSLDT 23
DB 25 HEPKGYHANFCLGCPPIYMSLDT 47

RESULT 4
AAR04075
ID AAR04075 standard; protein; 51 AA.

XX AAR04075;

XX 25-MAR-2003 (revised)
XX 31-OCT-2002 (revised)

XX 31-MAY-1989 (first entry)

XX Sequence of genomic fragment encoding a TGF-beta 1 exon.

XX Transforming growth factor beta-3 (TGF beta 3); tumour cells;
XX growth inhibition.

XX Homo sapiens.
OS
XX MO9912101-A.
XX
XX 14-DEC-1989.
XX
XX 08-JUN-1988; 88WO-US001945.
XX
XX 08-JUN-1988; 88WO-US001945.
XX
XX (GETH) GENENTECH INC.
XX
XX Derynck RMA, Goeddel DV;
XX
XX WPI, 1990-007474/01.
XX
XX P-PSDB; AAR04075.
XX
XX Nucleotide sequence encoding transforming growth factor beta-3 - used as
XX
XX a probe, or to produce tgf beta-3, for growth inhibition of certain
XX
XX normal and neoplastic cells, e.g. A549.
XX
XX
XX Disclosure; Fig 2; 61pp; English.
XX
XX
XX This sequence encodes an exon of transforming growth factor-beta 1 (TGF-
XX
XX beta 1) polypeptide corresponding to AA's 288-338 of mature TGF-beta 1.
XX
XX The nucleic acid sequence encoding the second subtype of TGF-beta (TGF-
XX
XX beta 3) is useful as a probe or to produce TGF-beta 3 for both normal and
XX
XX neoplastic cell growth inhibition. (Updated on 31-OCT-2002 to add missing
XX
XX OS field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-
XX
XX MAR-2003 to correct PI field.)
XX
XX
XX Sequence 51 AA;
XX
XX
XX

Query Match 100.0%; Score 145; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 8.9e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HEPKGYHANFCLGCPYIWSLDT 23
DB 25 HEPKGYHANFCLGCPYIWSLDT 47

RESULT 5
AAW78788
ID AAW78788 standard; protein, 51 AA.
XX
XX AAW78788;
XX
XX 25-MAR-2003 (revised)
XX
XX 21-DEC-1998 (first entry)
XX
XX Human transforming growth factor-beta fragment (aa288-338).
XX
XX
XX Transforming growth factor-beta 1, TGF-beta 1; human.
XX
XX Homo sapiens.
XX
XX US5801231-A.
XX
XX
XX 01-SEP-1998.
XX
XX
XX 30-MAY-1995; 95US-00454468.
XX
XX
XX 22-MAR-1985; 85US-00715142.
XX
XX 13-MAR-1987; 87US-00025423.
XX
XX 04-AUG-1989; 89US-00389929.
XX
XX 04-MAR-1992; 92US-00845893.
XX
XX 05-NOV-1993; 93US-00147364.
XX
XX (GETH) GENENTECH INC.
XX
XX Derynck RMA, Goeddel DV;
XX
XX
XX

XX WPI, 1998-494840/42.
XX
XX N-PSDB; AAV52936.
XX
XX
XX DNA encoding transforming growth factor-beta precursor sequence - useful
XX
XX for analysis to perform manipulations to increase yield of recombinant
XX
XX production of the protein.
XX
XX
XX Example 2; Fig 2; 26pp; English.
XX
XX

CC This polypeptide comprises amino acid residues 288-338 of human
CC
CC transforming growth factor-beta 1 precursor (preTGF-beta 1, see also
CC
CC AAW78785). It is encoded by an isolated fragment (see AAV52936) of the
CC
CC TGF-beta 1 gene. The invention relates to the recombinant production of
CC
CC TGF-beta. Nucleic acids encoding TGF-beta have been isolated and cloned
CC
CC into vectors which are replicated in bacteria and expressed in eukaryotic
CC
CC cells. TGF-beta recovered from transformed cells is used in known
CC
CC therapeutic applications. (Updated on 25-MAR-2003 to correct PF field.)
CC
XX
XX Sequence 51 AA;
XX
XX

Query Match 100.0%; Score 145; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 8.9e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HEPKGYHANFCLGCPYIWSLDT 23
DB 25 HEPKGYHANFCLGCPYIWSLDT 47

RESULT 6
ABB43879
ID ABB43879 standard; peptide, 51 AA.
XX
XX
XX ABB43879;
XX
XX
XX 04-FEB-2002 (first entry)
XX
XX
XX Peptide #11365 encoded by human foetal liver single exon probe.
XX
XX
XX Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
XX
XX Homo sapiens.
XX
XX
XX WO200157277-A2.
XX
XX
XX 09-AUG-2001.
XX
XX
XX 30-JAN-2001; 2001WO-US000669.
XX
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX
XX WPI; 2001-483447/52.
XX
XX
XX
XX Claim 27; SEQ ID NO 36514; 639pp + Sequence listing; English.
XX
XX
XX The invention relates to a single exon nucleic acid probe for measuring
XX
XX human gene expression in a sample derived from human foetal liver. The
XX
XX single exon nucleic acid probes may be used for predicting, measuring and
XX
XX displaying gene expression in samples derived from human foetal liver. The
XX
XX

CC present sequence is a peptide encoded by a single exon nucleic acid probe
 CC of the invention. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 51 AA;

Query Match 100.0%; Score 145; DB 4; Length 51;
 Best Local Similarity 100.0%; Pred. No. 8.9e-12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HEPKGYHANFCLGCPYIWSLDT 23
 |||||
 DB 25 HEPKGYHANFCLGCPYIWSLDT 47

RESULT 7
 AAM37799 ID AAM37799 standard; protein; 51 AA.

XX AAM37799;

DT 17-OCT-2001 (first entry)

DE Peptide #11836 encoded by probe for measuring placental gene expression.

XX Probe; microarray; human; placenta; antenatal diagnosis;

KM genetic disorder.

OS Homo sapiens.

XX WO200157272-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000663.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX DR WPI; 2001-488897/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human placenta.

XX PS Claim 27; SEQ ID NO 38068; 654bp; English.

XX CC The present invention relates to single exon nucleic acid probes (SENP:

XX CC see AAI31315-AA157546). The present sequence is a peptide encoded by one

XX CC such probe. The probes are useful for producing a microarray for

XX CC predicting, measuring and displaying gene expression in samples derived

XX CC from human placenta. The probes are useful for antenatal diagnosis of

XX CC human genetic disorders

XX SQ Sequence 51 AA;

Query Match 100.0%; Score 145; DB 4; Length 51;
 Best Local Similarity 100.0%; Pred. No. 8.9e-12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HEPKGYHANFCLGCPYIWSLDT 23
 |||||
 DB 25 HEPKGYHANFCLGCPYIWSLDT 47

RESULT 8
 AAM77605 ID AAM77605 standard; protein; 51 AA.

XX AAM77605;

Query Match 100.0%; Score 145; DB 4; Length 51;
 Best Local Similarity 100.0%; Pred. No. 8.9e-12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HEPKGYHANFCLGCPYIWSLDT 23
 |||||
 DB 25 HEPKGYHANFCLGCPYIWSLDT 47

RESULT 9
 ABG46640 ID ABG46640 standard; peptide; 51 AA.

XX ABG46640;

DT 19-AUG-2002 (first entry)

DE Human peptide encoded by genome-derived single exon probe SEQ ID 36305.

XX Human, single exon probe; asthma; lung cancer; COPD; ILD;

XX KM chronic obstructive pulmonary disease; interstitial lung disease;

XX KM familial idiopathic pulmonary fibrosis; neurofibromatosis;

XX KM tuberculous sclerosis; Gaucher's disease; Niemann-Pick disease;

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

XX DR WPI; 2001-488900/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human bone marrow.

XX PS Example 4; SEQ ID NO 37911; 658bp + Sequence Listing; English.

XX CC The present invention provides a number of single exon nucleic acid

XX CC probes which are derived from genomic sequences expressed in the human

XX CC bone marrow. They can be used to measure gene expression in bone marrow

XX CC samples, which may enable the improved diagnosis and treatment of cancers

XX CC such as lymphoma, leukemia and myeloma. The present sequence is a

XX CC protein encoded by one of the probes of the invention

XX CC

XX SQ Sequence 51 AA;

Query Match 100.0%; Score 145; DB 4; Length 51;
 Best Local Similarity 100.0%; Pred. No. 8.9e-12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HEPKGYHANFCLGCPYIWSLDT 23
 |||||
 DB 25 HEPKGYHANFCLGCPYIWSLDT 47

KM Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KM pulmonary histiocytosis; lymphangioleiomyomatosis; Karsageners syndrome;
 KM pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KM primary ciliary dyskinesia; pulmonary hypertension;
 KM hyaline membrane disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200186003-A2.
 PN
 XX 15-NOV-2001.
 PD
 XX 30-JAN-2001; 2001WO-US0000665.
 PF
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2002-114183/15.
 XX
 PT Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 PS
 XX Claim 27; SEQ ID NO 36305; 634bp; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC; the novel set of probes which hybridise at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exon should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karsageners syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a peptide/protein encoded by a single exon probe of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 51 AA;

Query Match 100.0%; Score 145; DB 5; Length 51;
 Best Local Similarity 100.0%; Pred. No. 8,9e-12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HEPKGYHANFCLGPPCYIWSLDT 23
 |||||
 Db 25 HEPKGYHANFCLGPPCYIWSLDT 47
 |||||
 RESULT 10
 AAB68685
 ID AAB68685 standard; protein; 60 AA.
 XX
 AC AAB68685;
 DT 03-MAY-2001 (first entry)
 XX
 DE Human TGFbeta1 protein #1.
 XX
 KW Human, transforming growth factor beta2; TGFbeta2; SELEX;
 KW systemic evolution of ligands by exponential enrichment.
 XX
 OS Homo sapiens.
 XX
 XX WO200109156-A1.
 PN
 PD 08-FEB-2001.
 XX
 PF 26-JUL-2000; 2000WO-US020397.
 PR 29-JUL-1999; 99US-00363939.
 XX
 PA (NEXS-) NEXSTAR PHARM INC.
 XX
 PI Pagratris N, Lochrie M, Gold L;
 XX WPI; 2001-218217/22.
 DR
 XX New RNA ligand to human transforming growth factor beta2, useful as
 PT pharmaceuticals, diagnostics and as immunohistochemical reagents.
 PT
 XX Disclosure; Page 71; 178bp; English.
 PS
 XX
 CC The present invention relates to non-naturally occurring, high-affinity
 CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
 CC oligonucleotide ligands were identified by the SELEX method (SELEX stands
 CC for Systemic Evolution of Ligands by Exponential Enrichment). The
 CC oligonucleotide ligands are useful in any process in which binding to
 CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
 CC diagnostics, imaging agents and immunohistochemical reagents
 CC
 XX
 SQ Sequence 60 AA;
 Query Match 100.0%; Score 145; DB 4; Length 60;
 Best Local Similarity 100.0%; Pred. No. 1e-11;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HEPKGYHANFCLGPPCYIWSLDT 23
 |||||
 Db 34 HEPKGYHANFCLGPPCYIWSLDT 56
 |||||
 RESULT 11
 AAM30331
 ID AAM30331 standard; peptide; 62 AA.
 XX
 AC AAM30331;
 DT 11-FEB-1998 (first entry)
 XX
 DE Fragment of growth factor TGFbeta1.
 XX

KW Neurturin; human; haematopoietic cell; neuronal cell; stem cell; NT gene;
 KW neurodegenerative disease; peripheral neuropathy; nervous system tumour;
 KW amyotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; ischaemic stroke; acute brain injury; basopenia;
 KW acute spinal cord injury; multiple sclerosis; eosinopenia; lymphopenia;
 KW monocytopenia; neutropenia; anaemia; thrombocytopenia; neuroblastoma;
 KW antibody; obesity; therapy; transforming growth factor beta; TGFbeta1;
 KW growth factor; hybrid protein.
 XX
 OS Homo sapiens.
 XX
 PN WO9708196-A1.
 XX
 PD 06-MAR-1997.
 XX
 PF 27-AUG-1996; 96WO-US014065.
 XX
 PR 28-AUG-1995; 95US-00519777.
 XX
 PA (UNIV) UNIV WASHINGTON.
 XX
 PI Johnson EM, Milbrandt JD, Kotzbauer PT, Lampe PA;
 DR WPI; 1997-179176/16.
 XX
 PT A novel growth factor Neurturin - used to treat neuro-degenerative and
 PT haematopoietic cell degeneration diseases, e.g. Alzheimer's disease and
 PT eosinopenia.
 XX
 PS Claim 93; Fig 17; 206pp; English.
 XX
 SQ AAW30331-W30353 represent human growth factor fragments that are used in
 CC a hybrid polypeptide of the invention. These sequences form a hybrid with
 CC the human neurturin (NT) fragment shown in AAW30378. NT promotes the
 CC growth and differentiation of haematopoietic and neuronal cells, and
 CC their stem cells. The NT gene and protein are used to prevent or treat
 CC neurodegenerative diseases e.g. peripheral neuropathy, amyotrophic
 CC lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's
 CC disease, ischaemic stroke, acute brain injury, acute spinal cord injury,
 CC nervous system tumour, multiple sclerosis and infection; and
 CC haematopoietic cell degenerative diseases, e.g. eosinopenia, basopenia,
 CC lymphopenia, monocytopenia, neutropenia, anaemia, thrombocytopenia,
 CC and stem cell insufficiencies. The NT protein and gene are also useful to
 CC treat neuroblastomas. Antibodies against NT and oligonucleotides (used as
 CC either probes or primers, corresponding to an exon of pre-pro-NT gene or
 CC flanking a target sequence) can be used for detecting NT in a sample or
 CC detecting mutations in the NT gene. Antisense sequences of the NT gene
 CC are used to treat diseases promoted by NT expression e.g. obesity
 XX
 SQ Sequence 62 AA;
 Query Match 100.0%; Score 145; DB 2; Length 62;
 Best Local Similarity 100.0%; Pred. No. 1.1e-11;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 HEPKGYHANFCLGCPPIYMSLDT 23
 |||||
 Db 20 HEPKGYHANFCLGCPPIYMSLDT 42
 |||||
 RESULT 12
 AAR22135 ID AAR22135 standard; peptide; 65 AA.
 XX
 AC AAR22135;
 XX
 DT 25-MAR-2003 (revised)
 DT 10-JUL-1992 (first entry)
 XX
 DB PDGI subunit b.
 XX
 KW Platelet derived growth inhibitor alpha; TGF-beta; trypsin; pepsin;
 KW cell proliferation; eczema; immunosuppressant.

XX
 OS Homo sapiens.
 XX
 PN EP475719-A.
 XX
 PD 18-MAR-1992.
 XX
 PF 10-SEP-1991; 91EP-00308239.
 XX
 PR 11-SEP-1990; 90JP-00238944.
 XX
 PA (NAKA/) NAKAMURA T.
 XX
 PI Nakamura T, Nakamura T;
 DR WPI; 1992-09304/12.
 XX
 PT New platelet-derived growth regulating peptide-alpha - used for treatment
 PT of eczema, stimulation of bone growth and as immunosuppressant.
 XX
 PS Claim 2; Page 11; 21pp; English.
 XX
 CC The peptide is subunit b of PDGI alpha. It can be obt'd. by treating
 CC transforming growth factor (TGF) beta with chymotrypsin or pepsin, or can
 CC be isolated from human blood platelets or by recombinant expression of
 CC DNA obt'd. using RNA ext'd. from blood plasma. PDGI alpha is comprised of
 CC subunits a, b and c bonded b-a-c. PDGI alpha can be used for controlling
 CC cell proliferation without the cancerous activity (transformation
 CC activity) associated with TGF-beta. PDGI- alpha can be used for
 CC activation and acceleration of the proliferation of epithelium cells in
 CC treating eczema, for stimulating osseous growth for bone formation or as
 CC an immuno- suppressant for immune diseases. See also AAR22134-6. (Updated
 CC on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 65 AA;
 Query Match 100.0%; Score 145; DB 2; Length 65;
 Best Local Similarity 100.0%; Pred. No. 1.1e-11;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 HEPKGYHANFCLGCPPIYMSLDT 23
 |||||
 Db 34 HEPKGYHANFCLGCPPIYMSLDT 56
 |||||
 RESULT 13
 AAY16697 ID AAY16697 standard; peptide; 98 AA.
 XX
 AC AAY16697;
 XX
 DT 17-AUG-1999 (first entry)
 DT 09-SEP-1999
 DE WO9914235 Seq ID No: 150.
 XX
 KW Growth factor; GF; perlepin; neuron growth; cellular degeneration;
 KW peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; trauma;
 KW brain injury; spinal cord injury; nervous system tumour; infection;
 KW multiple sclerosis; cardiac muscle degeneration; injury; neurotoxin;
 KW metabolic disease; diabetes; renal dysfunction; neurturin.
 XX
 OS Unidentified.
 XX
 PN WO9914235-A1.
 XX
 PD 25-MAR-1999.
 XX
 PF 15-SEP-1998; 98WO-US019163.
 XX
 PR 16-SEP-1997; 97US-00931858.
 XX
 PA (UNIV) UNIV WASHINGTON.

XX Johnson EM, Milbrandt JD, Kotzbauer PT, Lampe PA, Klein R;
PI Desauvage F;
XX WPI; 1999-244023/20.
XX
XX New isolated perlephin growth factor nucleic acids used to, e.g. promote
PT neuronal growth.
XX
XX Disclosure; Page 175-176; 222pp; English.
XX
XX The invention relates to a novel isolated and purified growth factor (GF)
CC that comprises perlephin or a fragment or a conservatively substituted
CC variant. The perlephin GF polypeptides can promote the survival and
CC growth of neurons and non-neuronal cells. The perlephin GF polypeptides
CC or polynucleotides can be used for preventing or treating cellular
CC degeneration or insufficiency, e.g. neuronal degeneration resulting from
CC peripheral neuropathy, amyotrophic lateral sclerosis, Alzheimer's
CC disease, Parkinson's disease, Huntington's disease, ischemic stroke,
CC acute brain injury, acute spinal cord injury, nervous system tumors,
CC multiple sclerosis, or infection, hematopoietic cell degeneration or
CC insufficiency resulting from eosinopenia, anemias, thrombocytopenia, or
CC stem-cell insufficiencies, cardiac muscle degeneration or insufficiency
CC resulting from cardiomyopathy or congestive heart failure. They can also
CC be used for treating e.g. peripheral nerve trauma or injury, exposure to
CC neurotoxins, metabolic diseases such as diabetes or renal dysfunctions
CC and damage caused by infectious agents. The GF can also be used for
CC promoting the growth and/or differentiation of a cell in a culture
CC medium. The antisense polynucleotides can be used for treating a disease
CC condition mediated by expression of perlephin by a population of cells.
CC The products can also be used for detection and diagnosis
XX
SQ Sequence 98 AA;
Query Match 100.0%; Score 145; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HEPKGYHANFCLGCPYIWSIDT 23
DB 20 HEPKGYHANFCLGCPYIWSIDT 42
RESULT 14
AAAY92554
ID AA92554 standard; peptide; 98 AA.
XX
XX AA92554;
XX
XX 10-AUG-2000 (first entry)
XX
XX TGB-beta 1 finger-1-heel-finger-2 sequence.
XX
XX finger domain; heel region; BMP; TGF-beta family; protein refolding;
XX fusion protein; osteopontin; antibacterial; cytoskeletal.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 2..29
XX /label= finger_1
XX /label= heel
XX /label= heel
XX /label= heel
XX /label= finger_2
XX
XX WO200020449-A2.
XX
XX 13-APR-2000.
XX
XX 07-OCT-1999; 99WO-US023372.
XX
XX 07-OCT-1998; 98US-0103418P.
XX
XX 07-OCT-1998; 98US-0103418P.
XX

PR 16-AUG-1999; 99US-00375333.
XX
XX (STYC) STRYKER CORP.
XX
XX Oppermann H, Tai M, McCartney J;
XX WPI; 2000-303743/26.
XX
XX A biologically active TGF-beta family member fusion protein competent to
PT refold, comprising a C-terminal linked TGF-beta family protein.
XX
XX Disclosure; Page 137-138; 160pp; English.
XX
XX AA92554-82 show the finger 1, heel and finger 2 domains of TGF-beta
CC superfamily members. These sequences can be used to form novel fusion
CC proteins. Novel proteins comprise biologically active TGF-beta family
CC member fusion proteins competent to refold under suitable refolding
CC conditions. The fusion proteins comprise: (1) a TGF-beta family protein C
CC -terminal seven cysteine domain, comprising finger 1, finger 2 and heel
CC subdomains; and (2) a heterologous leader sequence domain operatively
CC linked to the C-terminal domain. Truncations, heterodimers and mutants of
CC these fusion proteins and methods of purifying the heterodimers are also
CC claimed. The TGF-beta family proteins can be used to induce the full
CC cascade of morphogenic events which culminate in skeletal tissue
CC formation, including cartilage and endochondral bone formation. They are
CC useful in the binding of fibrin and fibronectin to the implanted matrix,
CC chemotaxis of cells, proliferation of fibroblasts, differentiation into
CC chondroblasts, cartilage formation, vascular invasion, bone formation,
CC remodeling, and bone marrow differentiation. The proteins have improved
CC physical properties such as solubility and stability, improved biological
CC activity, including altered receptor binding and improved targeting
XX
XX capabilities
XX
SQ Sequence 98 AA;
Query Match 100.0%; Score 145; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HEPKGYHANFCLGCPYIWSIDT 23
DB 20 HEPKGYHANFCLGCPYIWSIDT 42
RESULT 15
AAB09519
ID AAB09519 standard; protein; 98 AA.
XX
XX AAB09519;
XX
XX 11-SEP-2000 (first entry)
XX
XX Human TGF-beta 1, SEQ ID NO:40.
XX
XX TGF-beta superfamily; transforming growth factor-beta;
XX developmental regulation; finger 2 subdomain; basic region;
XX protein refolding; stability; solubility; osteogenic protein; OP;
XX bone morphogenetic protein; BMP; growth/differentiation factor; GDF;
XX inhibin; tissue morphogenesis; regeneration; bone; dental tissue;
XX connective tissue; cartilage; vunerary.
XX
XX Homo sapiens.
XX
XX WO200020607-A2.
XX
XX 13-APR-2000.
XX
XX 07-OCT-1999; 99WO-US023371.
XX
XX 07-OCT-1998; 98US-0103418P.
XX
XX 16-AUG-1999; 99US-00374958.
XX
XX (STYC) STRYKER CORP.
XX

XX Oppermann H, Tai M, McCartney J;
 PI
 XX WPI: 2000-303787/26.
 DR N-PSDB; AAA38544.
 XX

PT Transforming growth factor-beta superfamily member mutant induces tissue
 PT morphogenesis in e.g. bone, non-mineralized skeletal tissue, dental
 PT tissue and connective tissue and comprises a substitution in a region of
 PT the finger 2 domain.

XX
 PS Claim 14; Page 140; 162pp; English.

XX
 CC The invention relates to mutant TGF-beta (transforming growth factor-
 CC beta) superfamily members. These mutants comprise one or more amino acid
 CC substitutions in the base region of the finger 2 subdomain, and a C-
 CC terminal residue selected from Arg, Ile, Leu, Ser and Ala. In the finger
 CC 2 subdomain, basic residues (e.g., Arg, Lys), or residues containing an
 CC amide group (e.g., Gln, Asn), are substituted with acidic residues (e.g.,
 CC Glu, Asp) or residues containing a hydroxyl group (e.g., Ser, Thr). TGF-
 CC beta superfamily proteins regulate developmental processes and include
 CC proteins such as the osteogenic proteins (OPs), bone morphogenetic
 CC proteins (BMPs), growth/differentiation factors (GDFs) and inhibins.
 CC Specific examples of TGF-beta superfamily mutants encompassed by the
 CC invention are the finger 2 subdomain mutants of human osteogenic protein-
 CC 1 (OP-1) (AAB09576-B09615). Mutant TGF-beta proteins are used for
 CC inducing tissue morphogenesis in bone, non-mineralised skeletal tissue,
 CC dental tissue, connective tissue, brain, liver and nerve tissue. The
 CC proteins can be used in conjunction with a biocompatible matrix e.g.,
 CC collagen, hydroxyapatite or carboxymethylcellulose for regenerating bone,
 CC cartilage and/or other mineralised skeletal or connective tissues e.g.,
 CC ligament, tendon, muscle, fibrocartilage, joint capsule and
 CC intervertebral discs. The OP-1 mutants can be used to repair diseased or
 CC damaged mammalian tissue and to prevent or substantially inhibit
 CC immune/inflammatory response-mediated tissue damage and scar tissue
 CC formation following an injury. Compared to the wild-type TGF-beta
 CC superfamily members, the mutant proteins have improved in vitro refolding
 CC properties in a pH range of 6-9, increased solubility in aqueous solution
 CC and improved stability and/or activity. Sequences AAB09519-B09542 and
 CC AAB09553-B09558 represent a variety of wild-type TGF-beta superfamily
 CC proteins referred to in the specification

XX
 SQ Sequence 98 AA;

Query Match 100.0%; Score 145; DB 3; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.6e-11;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGPPYIWSLDT 23
 |||||
 DB 20 HEPKGYHANFCLGPPYIWSLDT 42

Search completed: June 14, 2005, 15:46:23
 Job time : 131.808 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2005, 15:46:34 ; Search time 34.0577 Seconds
(without alignments)
50.412 Million cell updates/sec

Title: US-09-831-253F-10
Perfect score: 145
Sequence: 1 HEPKGYHANFCLGPPCYIWSLDT 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfill1es1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	145	100.0	51	5168051-4	Patent No. 5168051
2	145	100.0	51	5168051-4	Patent No. 5168051
3	145	100.0	60	US-09-363-939A-122	Sequence 122, App
4	145	100.0	60	US-09-791-301-122	Sequence 122, App
5	145	100.0	70	US-09-848-664A-9	Sequence 9, Appl1
6	145	100.0	98	US-08-478-097A-1	Sequence 1, Appl1
7	145	100.0	98	US-08-931-858E-150	Sequence 150, App
8	145	100.0	98	US-08-981-739-150	Sequence 150, App
9	145	100.0	98	US-09-128-026-150	Sequence 150, App
10	145	100.0	98	US-09-496-398-1	Sequence 1, Appl1
11	145	100.0	98	US-09-220-616-150	Sequence 150, App
12	145	100.0	98	US-09-374-958C-40	Sequence 40, App
13	145	100.0	98	US-09-220-527-150	Sequence 150, App
14	145	100.0	98	US-09-220-407-150	Sequence 150, App
15	145	100.0	112	US-07-979-441-1	Sequence 1, Appl1
16	145	100.0	112	US-08-197-793-36	Sequence 36, Appl1
17	145	100.0	112	US-08-486-057B-41	Sequence 41, Appl1
18	145	100.0	112	US-08-459-850-36	Sequence 36, Appl1
19	145	100.0	112	US-08-459-214-36	Sequence 36, Appl1
20	145	100.0	112	US-08-470-837-30	Sequence 30, Appl1
21	145	100.0	112	US-08-789-588-41	Sequence 41, Appl1
22	145	100.0	112	US-08-410-573-1	Sequence 1, Appl1
23	145	100.0	112	US-09-123-233-2	Sequence 2, Appl1
24	145	100.0	112	US-08-927-433-5	Sequence 5, Appl1
25	145	100.0	112	US-08-868-452-30	Sequence 30, Appl1
26	145	100.0	112	US-09-095-637D-1	Sequence 1, Appl1
27	145	100.0	112	PCT-US93-03068-1	Sequence 1, Appl1

28	145	100.0	114	1	US-08-481-377-23	Sequence 23, Appl1
29	145	100.0	114	2	US-08-491-835-21	Sequence 21, Appl1
30	145	100.0	114	3	US-09-153-733A-23	Sequence 23, Appl1
31	145	100.0	114	3	US-08-946-092A-21	Sequence 21, Appl1
32	145	100.0	114	3	US-09-172-062-21	Sequence 21, Appl1
33	145	100.0	114	3	US-08-624-635-22	Sequence 22, Appl1
34	145	100.0	114	3	US-09-301-520D-21	Sequence 21, Appl1
35	145	100.0	114	3	US-09-389-705-23	Sequence 23, Appl1
36	145	100.0	114	5	PCT-US94-00666-23	Sequence 23, Appl1
37	145	100.0	114	5	PCT-US94-00685-21	Sequence 21, Appl1
38	145	100.0	115	1	US-08-581-529B-19	Sequence 19, Appl1
39	145	100.0	115	1	US-08-455-559-25	Sequence 25, Appl1
40	145	100.0	115	2	US-08-525-596B-29	Sequence 29, Appl1
41	145	100.0	115	2	US-08-581-528A-19	Sequence 19, Appl1
42	145	100.0	115	3	US-09-097-616-19	Sequence 19, Appl1
43	145	100.0	115	3	US-09-177-860A-29	Sequence 29, Appl1
44	145	100.0	115	3	US-09-145-060-25	Sequence 25, Appl1
45	145	100.0	115	4	US-09-378-238-39	Sequence 39, Appl1

ALIGNMENTS

```

RESULT 1
5168051-4
; Patent No. 5168051
; APPLICANT: DERYNCK, RIK M.A.; GOEDEL, DAVID V.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/389,929
; FILING DATE: 04-AUG-1989
; SEQ ID NO.4:
; LENGTH: 51
; 5168051-4

Query Match
Best Local Similarity 100.0%; Score 145; DB 6; Length 51;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 HEPKGYHANFCLGPPCYIWSLDT 23
|||||
25 HEPKGYHANFCLGPPCYIWSLDT 47

Db
25 HEPKGYHANFCLGPPCYIWSLDT 47

RESULT 2
5168051-4
; Patent No. 5168051
; APPLICANT: DERYNCK, RIK M.A.; GOEDEL, DAVID V.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/389,929
; FILING DATE: 04-AUG-1989
; SEQ ID NO.4:
; LENGTH: 51
; 5168051-4

Query Match
Best Local Similarity 100.0%; Score 145; DB 6; Length 51;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 HEPKGYHANFCLGPPCYIWSLDT 23
|||||
25 HEPKGYHANFCLGPPCYIWSLDT 47

Db
25 HEPKGYHANFCLGPPCYIWSLDT 47

RESULT 3
US-09-363-939A-122
; Sequence 122, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
; APPLICANT: Pagratlis, Nikos

```

```

; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX87
; CURRENT APPLICATION NUMBER: US/09/363,939A
; CURRENT FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-363-939A-122

```

```

Query Match          100.0%; Score 145; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 HEPKGYHANFCLGCPYIWSLDT 23
        |||||||||||||||||||
Db      34 HEPKGYHANFCLGCPYIWSLDT 56

```

```

RESULT 4
US-09-791-301-122
; Sequence 122, Application US/09791301
; Patent No. 6713616
; GENERAL INFORMATION:
; APPLICANT: Pagratlis, Nikos
; APPLICANT: Lochrie, Michael
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; FILE REFERENCE: NEX 87/C
; CURRENT APPLICATION NUMBER: US/09/791,301
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; PRIOR APPLICATION NUMBER: 09/363,939
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122

```

```

; LENGTH: 60
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-791-301-122

```

```

Query Match          100.0%; Score 145; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 HEPKGYHANFCLGCPYIWSLDT 23
        |||||||||||||||||||
Db      34 HEPKGYHANFCLGCPYIWSLDT 56

```

```

RESULT 5
US-09-848-664A-9
; Sequence 9, Application US/09848664A
; Patent No. 6723344
; GENERAL INFORMATION:
; APPLICANT: Sakiyama-Eibert, Shelly E.
; APPLICANT: Hubbell, Jeffrey A.
; TITLE OF INVENTION: Controlled Release of No. 6723344-Heparin Binding Growth
; FILE REFERENCE: ETH 108
; CURRENT APPLICATION NUMBER: US/09/848,664A
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US/09/298,084A
; PRIOR FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-848-664A-9

```

```

Query Match          100.0%; Score 145; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 3e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 HEPKGYHANFCLGCPYIWSLDT 23
        |||||||||||||||||||
Db      34 HEPKGYHANFCLGCPYIWSLDT 56

```

```

RESULT 6
US-08-478-097A-1
; Sequence 1, Application US/08478097A
; Patent No. 6040431
; GENERAL INFORMATION:
; APPLICANT: KECK, PETER
; APPLICANT: SMART, JOHN
; TITLE OF INVENTION: SINGLE-CHAIN ANALOGS OF TGF-B
; TITLE OF INVENTION: SUPERFAMILY (MORPHONS)
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HUMWITZ &
; ADDRESSEE: THIBEAULT, LLP
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,097A

```


FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-080
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..98
OTHER INFORMATION: /note= "TGF-B1 SEQUENCE"
US-08-478-097A-1

Query Match 100.0%; Score 145; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 20 HEPKGYHANFCLGCPYIWSLDT 42

RESULT 7
US-08-931-858E-150
Sequence 150, Application US/08931858E
Patent No. 6222022
GENERAL INFORMATION:
APPLICANT: JOHNSON, EUGENE M
APPLICANT: MILBRANDT, JEFFREY D
APPLICANT: KOTZBAUER, PAUL T
APPLICANT: LAMPE, PATRICIA A
APPLICANT: KLEIN, ROBERT
APPLICANT: DESAUVAGE, FRED
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931.858E
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971486
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-931-858E-150

Query Match 100.0%; Score 145; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 20 HEPKGYHANFCLGCPYIWSLDT 42

RESULT 8
US-08-981-739-150
Sequence 150, Application US/08981739
Patent No. 6232449
GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: LAMPE, PATRICIA A.
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981.739
FILING DATE: 31-Aug-1998
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/03461
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976163
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 150:
US-08-981-739-150

Query Match 100.0%; Score 145; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 20 HEPKGYHANFCLGCPYIWSLDT 42

RESULT 9
US-09-128-026-150
Sequence 150, Application US/09128026
Patent No. 6403335
GENERAL INFORMATION:

APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: LAMPE, PATRICIA A.
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,026
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976163
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-128-026-150

Query Match 100.0%; Score 145; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 4,2e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPPIYMSLDT 23
Db 20 HEPKGYHANFCLGCPPIYMSLDT 42

RESULT 10
US-09-496-398-1
Sequence 1, Application US/09496398
Patent No. 6479643
GENERAL INFORMATION:
APPLICANT: KECK, PETER
APPLICANT: SMART, JOHN
TITLE OF INVENTION: SINGLE CHAIN ANALOGS OF TGF-B
TITLE OF INVENTION: SUPERFAMILY (MORPHONS)
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HURWITZ &
STREET: THIBEAULT, LLP
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/496,398
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,097
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STK-059CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..98
OTHER INFORMATION: /note= "TGF-B1 SEQUENCE"
US-09-496-398-1

Query Match 100.0%; Score 145; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 4,2e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPPIYMSLDT 23
Db 20 HEPKGYHANFCLGCPPIYMSLDT 42

RESULT 11
US-09-220-616-150
Sequence 150, Application US/09220616
Patent No. 6645937
GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: LAMPE, PATRICIA A.
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/220,616
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/981,739
FILING DATE: 31-Aug-1998
APPLICATION NUMBER: PCT/US97/03461
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976163
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092

INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-220-616-150

Query Match 100.0%; Score 145; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 20 HEPKGYHANFCLGCPYIWSLDT 42

RESULT 12
US-09-374-958C-40
Sequence 40, Application US/09374958C
Patent No. 6677432
GENERAL INFORMATION:
APPLICANT: Stryker Corporation
TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, including
FILE REFERENCE: STK-076
CURRENT APPLICATION NUMBER: US/09/374,958C
CURRENT FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PatentIn version 2.0
SEQ ID NO 40
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: TGF-beta1
US-09-374-958C-40

Query Match 100.0%; Score 145; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 20 HEPKGYHANFCLGCPYIWSLDT 42

RESULT 13
US-09-220-527-150
Sequence 150, Application US/09220527
Patent No. 6692943
GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
MILBRANDT, JEFFREY D.
KOTZBAUER, PAUL T.
LAMPE, PATRICIA A.
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESSES:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/220,527

FILING DATE: 24-Dec-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/981,739
FILING DATE: 31-Aug-1998
APPLICATION NUMBER: PCT/US97/03461
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976163
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 150:
US-09-220-527-150

Query Match 100.0%; Score 145; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 20 HEPKGYHANFCLGCPYIWSLDT 42

RESULT 14
US-09-220-407-150
Sequence 150, Application US/09220407
Patent No. 6716600
GENERAL INFORMATION:
APPLICANT: JOHNSON, EUGENE M.
MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: LAMPE, PATRICIA A.
APPLICANT: KLEIN, ROBERT
APPLICANT: DESAUVAGE, FRED
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESSES:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/220,407
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/931,858
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971486
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 150:

Job time : 34.0577 secs

SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-220-407-150

Query Match 100.0%; Score 145; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 20 HEPKGYHANFCLGCPYIWSLDT 42

RESULT 15
US-07-979-441-1
; Sequence 1, Application US/07979441
; Patent No. 5462925
; GENERAL INFORMATION:
; APPLICANT: OGAMA, YASUSHI
; APPLICANT: SCHMIDT, DAVID
; APPLICANT: DASCH, JAMES
; TITLE OF INVENTION: NOVEL BETA-TYPE TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/979,441
; FILING DATE: 19921120
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/614,306
; FILING DATE: 16-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 220952024800
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-979-441-1

Query Match 100.0%; Score 145; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 34 HEPKGYHANFCLGCPYIWSLDT 56

Search completed: June 14, 2005, 16:10:14

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2005, 15:51:20 ; Search time 120.308 Seconds
(without alignments)
73.285 Million cell updates/sec

Title: US-09-831-253F-10
Perfect score: 145
Sequence: 1 HEPKGYHANFCLGPCPYIWSLDT 23

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10A_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	145	100.0	51	9	US-09-864-761-47871
2	145	100.0	60	10	US-09-791-301-122
3	145	100.0	60	16	US-10-812-642-122
4	145	100.0	70	9	US-09-848-664-9
5	145	100.0	98	14	US-10-187-394-1
6	145	100.0	112	9	US-09-813-271B-2
7	145	100.0	112	15	US-10-366-345-54
8	145	100.0	112	17	US-10-872-198-104
9	145	100.0	113	9	US-09-813-398-13
10	145	100.0	113	16	US-10-826-324-13
11	145	100.0	114	9	US-09-389-705-23

12	145	100.0	114	9	US-09-813-459-22	Sequence 22, Appl
13	145	100.0	114	13	US-10-115-406-21	Sequence 21, Appl
14	145	100.0	114	14	US-10-154-333-23	Sequence 23, Appl
15	145	100.0	114	16	US-10-704-223-21	Sequence 21, Appl
16	145	100.0	115	9	US-09-859-211-47	Sequence 47, Appl
17	145	100.0	115	9	US-09-880-708-25	Sequence 25, Appl
18	145	100.0	115	10	US-09-872-856-47	Sequence 47, Appl
19	145	100.0	115	14	US-10-335-483-29	Sequence 29, Appl
20	145	100.0	115	15	US-10-463-973-47	Sequence 47, Appl
21	145	100.0	115	15	US-10-693-336-19	Sequence 19, Appl
22	145	100.0	115	16	US-10-758-210-19	Sequence 19, Appl
23	145	100.0	139	13	US-10-002-278-8	Sequence 8, Appl
24	145	100.0	185	16	US-10-781-866-52	Sequence 52, Appl
25	145	100.0	218	16	US-10-781-866-51	Sequence 51, Appl
26	145	100.0	315	10	US-09-214-592-25	Sequence 25, Appl
27	145	100.0	390	9	US-09-756-283A-23	Sequence 23, Appl
28	145	100.0	390	10	US-09-214-592-23	Sequence 20, Appl
29	145	100.0	390	10	US-09-214-592-23	Sequence 20, Appl
30	145	100.0	390	10	US-09-214-592-26	Sequence 26, Appl
31	145	100.0	390	10	US-09-214-592-28	Sequence 28, Appl
32	145	100.0	390	10	US-09-214-592-33	Sequence 29, Appl
33	145	100.0	390	10	US-09-214-592-33	Sequence 33, Appl
34	145	100.0	390	14	US-10-087-268-2	Sequence 2, Appl
35	145	100.0	390	14	US-10-087-268-5	Sequence 5, Appl
36	145	100.0	390	14	US-10-276-947-1	Sequence 1, Appl
37	145	100.0	390	14	US-10-131-985-13	Sequence 13, Appl
38	145	100.0	390	15	US-10-366-345-46	Sequence 46, Appl
39	145	100.0	390	16	US-10-746-845-38	Sequence 38, Appl
40	145	100.0	390	16	US-10-688-845-12	Sequence 12, Appl
41	145	100.0	390	17	US-10-741-600-1307	Sequence 1307, Ap
42	145	100.0	390	17	US-10-741-600-1308	Sequence 1308, Ap
43	145	100.0	390	17	US-10-901-417-13	Sequence 13, Appl
44	145	100.0	391	10	US-09-214-592-17	Sequence 17, Appl
45	145	100.0	391	17	US-10-741-600-1309	Sequence 1309, Ap

ALIGNMENTS

RESULT 1
US-09-864-761-47871
; Sequence 47871, Application US/09864761
; Patent No. US20020048763A1
GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Accm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30

```

; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47871
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011462.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.8
; OTHER INFORMATION: EST HUMAN HIT: BE737006.1, EVALUE 4.00e-28
; OTHER INFORMATION: SWISSPROT HIT: O19011, EVALUE 3.00e-29
US-09-864-761-47871

Query Match          100.0%; Score 145; DB 9; Length 51;
Best Local Similarity 100.0%; Pred. No. 2,7e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HEPKGYANFCLGCPYIWSLDT 23
Db      25 HEPKGYANFCLGCPYIWSLDT 47

RESULT 2
US-09-791-301-122
; Sequence 122, Application US/09791301
; Publication No. US2003006493A1
; GENERAL INFORMATION:
; APPLICANT: Pagratie, Nikos
; APPLICANT: Lochrie, Michael
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; FILE REFERENCE: NEX 87/C
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; PRIOR APPLICATION NUMBER: 09/363,939
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
```

```

; LENGTH: 60
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-791-301-122

Query Match          100.0%; Score 145; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HEPKGYANFCLGCPYIWSLDT 23
Db      34 HEPKGYANFCLGCPYIWSLDT 56

RESULT 3
US-10-812-642-122
; Sequence 122, Application US/10812642
; Publication No. US20040258656A1
; GENERAL INFORMATION:
; APPLICANT: Pagratie, Nikos
; APPLICANT: Lochrie, Michael
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; FILE REFERENCE: NEX87
; CURRENT FILING DATE: 2004-03-30
; PRIOR APPLICATION NUMBER: US/10/812,642
; PRIOR FILING DATE: 2004-03-30
; PRIOR APPLICATION NUMBER: US/09/363,939A
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-10-812-642-122

Query Match          100.0%; Score 145; DB 16; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HEPKGYANFCLGCPYIWSLDT 23
Db      34 HEPKGYANFCLGCPYIWSLDT 56

RESULT 4
US-09-848-664-9
; Sequence 9, Application US/09848664
; Patent No. US2002014641A1
; GENERAL INFORMATION:
; APPLICANT: Sakiyama-Eibert, Shelly E.
; APPLICANT: Hubbard, Jeffrey A.
```

TITLE OF INVENTION: Controlled Release of No. US2002014641A1-Heparin Binding Growth
; TITLE OF INVENTION: Factors from Heparin Containing Matrices
; FILE REFERENCE: ETH 108
; CURRENT APPLICATION NUMBER: US/09/848,664
; PRIOR APPLICATION NUMBER: 2001-05-03
; PRIOR FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 9
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-848-664-9

Query Match 100.0%; Score 145; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 3.5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 34 HEPKGYHANFCLGCPYIWSLDT 56

RESULT 5
US-10-187-394-1
; Sequence 1, Application US/10187394
; Publication No. US20030176667A1
; GENERAL INFORMATION:
; APPLICANT: KECK, PETER
; APPLICANT: SMART, JOHN
; TITLE OF INVENTION: SINGLE CHAIN ANALOGS OF TGF-B
; TITLE OF INVENTION: SUPERFAMILY (MORPHONS)
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESS: PATENT ADMINISTRATOR; TESTA, HURWITZ &
; ADDRESS: THIBEAULT, LLP
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/187,394
; FILING DATE: 28-JUNE-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/496,398
; FILING DATE: 02-FEB-2000
; CLASSIFICATION:
; APPLICATION NUMBER: US 08/478,097
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESO, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: STK-059CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7000
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:

NAME/KEY: Protein
; LOCATION: 1..98
; OTHER INFORMATION: /note="TGF-B1 SEQUENCE"
US-10-187-394-1

Query Match 100.0%; Score 145; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 20 HEPKGYHANFCLGCPYIWSLDT 42

RESULT 6
US-09-813-271B-2
; Sequence 2, Application US/09813271B
; Patent No. US20020115834A1
; GENERAL INFORMATION:
; APPLICANT: (A) Nisco Cerletti
; TITLE OF INVENTION: New process for the production of
; biologically active protein
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. US20020115834A1artis Patent Department
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,271B
; FILING DATE: 20-Mar-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/02719
; FILING DATE: 12-Jul-95
; APPLICATION NUMBER: EPO 94810439.3
; FILING DATE: 25-Jul-94
; ATTORNEY/AGENT INFORMATION:
; NAME: Pfeiffer, Hessa J.
; REGISTRATION NUMBER: 22640
; REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 522-6940
; TELEFAX: (908) 522-6955
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-813-271B-2

Query Match 100.0%; Score 145; DB 9; Length 112;
Best Local Similarity 100.0%; Pred. No. 5.3e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 34 HEPKGYHANFCLGCPYIWSLDT 56

RESULT 7
US-10-366-345-54
; Sequence 54, Application US/10366345
; Publication No. US20030224501A1

```
; GENERAL INFORMATION:
; APPLICANT: Young, et al.
; TITLE OF INVENTION: Bone Morphogenetic Protein Polynucleotides, Polypeptides and
; FILE REFERENCE: PT189
; CURRENT APPLICATION NUMBER: US/10/366,345
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-366-345-54

Query Match          100.0%; Score 145; DB 15; Length 112;
Best Local Similarity 100.0%; Pred. No. 5.3e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HEPKGYHANFCLGPGPYIWSLDT 23
        |||||||||||||||||||
Db      34 HEPKGYHANFCLGPGPYIWSLDT 56

RESULT 8
US-10-872-198-104
; Sequence 104, Application US/10872198
; Publication No. US2005002897A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreea SCHEIDIG
; APPLICANT: Christian VOETSMEIER
; APPLICANT: Ulrich Kettling
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.000204
; CURRENT APPLICATION NUMBER: US/10/872,198
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-198-104

Query Match          100.0%; Score 145; DB 17; Length 112;
Best Local Similarity 100.0%; Pred. No. 5.3e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HEPKGYHANFCLGPGPYIWSLDT 23
        |||||||||||||||||||
Db      34 HEPKGYHANFCLGPGPYIWSLDT 56

RESULT 9
US-09-813-398-13
; Sequence 13, Application US/09813398
; Patent No. US20020169292A1
; GENERAL INFORMATION:
; APPLICANT: Bruce D. Weintraub
```

```
; APPLICANT: Mariusz W. Szkudlinski
; APPLICANT: University of Maryland
; TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
; FILE REFERENCE: USFMD.003C1
; CURRENT APPLICATION NUMBER: US/09/813,398
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: PCT/US99/05908
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/US98/19772
; PRIOR FILING DATE: 1998-09-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 113
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
US-09-813-398-13

Query Match          100.0%; Score 145; DB 9; Length 113;
Best Local Similarity 100.0%; Pred. No. 5.3e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HEPKGYHANFCLGPGPYIWSLDT 23
        |||||||||||||||||||
Db      35 HEPKGYHANFCLGPGPYIWSLDT 57

RESULT 10
US-10-826-324-13
; Sequence 13, Application US/10826324
; Publication No. US20040265972A1
; GENERAL INFORMATION:
; APPLICANT: Bruce D. Weintraub
; APPLICANT: Mariusz W. Szkudlinski
; APPLICANT: University of Maryland
; TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
; FILE REFERENCE: USFMD.003C1
; CURRENT APPLICATION NUMBER: US/10/826,324
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US/09/813,398
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: PCT/US99/05908
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/US98/19772
; PRIOR FILING DATE: 1998-09-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 113
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
US-10-826-324-13

Query Match          100.0%; Score 145; DB 16; Length 113;
Best Local Similarity 100.0%; Pred. No. 5.3e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HEPKGYHANFCLGPGPYIWSLDT 23
        |||||||||||||||||||
Db      35 HEPKGYHANFCLGPGPYIWSLDT 57

RESULT 11
US-09-389-705-23
; Sequence 23, Application US/09389705
; Publication No. US20010018509A1
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLAY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
```


CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/389,705
FILING DATE: 03-Sep-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/153,733
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR., Ph.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD2279 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5100
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta 1
FEATURE:
NAME/KEY: Protein
LOCATION: 1..114
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-389-705-23
Query Match 100.0%; Score 145; DB 9; Length 114;
Best Local Similarity 100.0%; Pred. No. 5,4e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 36 HEPKGYHANFCLGCPYIWSLDT 58
RESULT 12
US-09-813-459-22
Sequence 22, Application US/09813459
Patent No. US20020107369A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
Cunningham, No. US20020107369A1
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,459
FILING DATE: 20-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/624,635
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John R.,
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-3054
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-1
FEATURE:
NAME/KEY: Protein
LOCATION: 1..114
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-813-459-22
Query Match 100.0%; Score 145; DB 9; Length 114;
Best Local Similarity 100.0%; Pred. No. 5,4e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 36 HEPKGYHANFCLGCPYIWSLDT 58

RESULT 13
US-10-115-406-21
Sequence 21, Application US/10115406
Publication No. US20020127612A1
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
FILE REFERENCE: JH01190-3
CURRENT APPLICATION NUMBER: US/10/115,406
PRIOR FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: 09/301,520
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: US 09/172,062
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 08/491,835
PRIOR FILING DATE: 1995-10-23
PRIOR APPLICATION NUMBER: PCT/US94/00685
PRIOR FILING DATE: 1994-01-12
PRIOR APPLICATION NUMBER: US 08/003,303
PRIOR FILING DATE: 1993-01-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
SEQ ID NO 21
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-115-406-21
Query Match 100.0%; Score 145; DB 13; Length 114;
Best Local Similarity 100.0%; Pred. No. 5,4e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 36 HEPKGYHANFCLGCPYIWSLDT 58
RESULT 14
US-10-154-333-23

```
; Sequence 23, Application US/10154333
; Publication No. US20030109684A1
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/154,333
; FILING DATE: 21-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/389,705
; FILING DATE: 03-Sep-1999
; APPLICATION NUMBER: 09/153,733
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERELL, JR. Ph. D., JOHN R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD2279 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta 1
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..114
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
; US-10-154-333-23

Query Match 100.0%; Score 145; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 5,4e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGPCPYIWSLDT 23
Db 36 HEPKGYHANFCLGPCPYIWSLDT 58

RESULT 15
US-10-704-223-21
; Sequence 21, Application US/10704223
; Publication No. US20040152143A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
; FILE REFERENCE: JHU1190-7
; CURRENT APPLICATION NUMBER: US/10/704,223
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 10/115,406
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US 09/301,520
; PRIOR FILING DATE: 1999-04-28
```

```
; PRIOR APPLICATION NUMBER: US 09/172,062
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 08/491,835
; PRIOR FILING DATE: 1995-10-23
; PRIOR APPLICATION NUMBER: PCT/US94/00685
; PRIOR FILING DATE: 1994-01-12
; PRIOR APPLICATION NUMBER: US 08/003,303
; PRIOR FILING DATE: 1993-01-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 21
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-704-223-21

Query Match 100.0%; Score 145; DB 16; Length 114;
Best Local Similarity 100.0%; Pred. No. 5,4e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGPCPYIWSLDT 23
Db 36 HEPKGYHANFCLGPCPYIWSLDT 58
```

Search completed: June 14, 2005, 16:14:52
Job time : 120.308 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2005, 15:35:40 ; Search time 25.6538 Seconds
(without alignments)
86.263 Million cell updates/sec

Title: US-09-831-253F-10
Perfect score: 145
Sequence: 1 HEPKGYHANFCLGCPYIWSLDT 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	145	100.0	130	2	148196	transforming growth
2	145	100.0	315	2	A40057	transforming growth
3	145	100.0	390	1	WFMU2	transforming growth
4	145	100.0	390	1	WFMU2	transforming growth
5	145	100.0	390	2	A26960	transforming growth
6	145	100.0	390	2	JC4023	transforming growth
7	145	100.0	390	2	A27512	transforming growth
8	145	100.0	390	2	146463	transforming growth
9	145	100.0	390	2	SI0219	transforming growth
10	145	100.0	390	2	SI0219	transforming growth
11	128	88.3	373	2	A41918	transforming growth
12	124	85.5	412	2	A34989	transforming growth
13	123	84.8	382	2	B61036	transforming growth
14	117	80.7	112	2	A61439	transforming growth
15	117	80.7	413	1	WFLB2	transforming growth
16	117	80.7	414	1	WFMU2	transforming growth
17	117	80.7	414	1	WFMU2	transforming growth
18	117	80.7	414	2	A31249	transforming growth
19	117	80.7	442	2	B31249	transforming growth
20	112	77.2	409	2	S01825	transforming growth
21	112	77.2	410	2	A41397	transforming growth
22	112	77.2	412	2	A36169	transforming growth
23	111	76.6	410	2	A35706	transforming growth
24	109	75.2	412	2	A34939	transforming growth
25	68	46.9	115	2	PM0504	activin beta A chain
26	68	46.9	360	2	A28619	Vg1 embryonic growth
27	68	46.9	424	1	B40905	inhibin beta-A chain
28	68	46.9	424	1	S31440	inhibin beta-A chain
29	68	46.9	424	1	WFMU2	inhibin beta-A chain

30	68	46.9	425	1	S50898	inhibin beta-A cha
31	68	46.9	425	2	I47072	inhibin beta-A cha
32	68	46.9	426	1	B24248	inhibin beta-A cha
33	67	46.2	102	2	A36192	inhibin beta-A cha
34	64	44.1	352	2	JC2456	inhibin beta-C cha
35	62	42.8	366	2	A45402	transforming growt
36	62	42.8	366	2	A46607	transforming growt
37	61	42.1	351	2	A34201	bone morphogenetic
38	61	42.1	352	2	S70580	bone morphogenetic
39	61	42.1	352	2	JC5366	activin beta C pre
40	61	42.1	393	2	S37073	bone morphogenetic
41	61	42.1	394	2	S45355	bone morphogenetic
42	61	42.1	396	1	EMH02	bone morphogenetic
43	61	42.1	398	2	JH0688	bone morphogenetic
44	61	42.1	398	2	JH0687	bone morphogenetic
45	60	41.4	367	2	JC4151	activin beta D cha

ALIGNMENTS

RESULT 1
148196
transforming growth factor beta-1 precursor - golden hamster (fragment)
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 02-Jul-1996 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004
C:Accession: 148196
R:Wong, D.T.; Donoff, R.B.; Yang, J.; Song, B.Z.; Matossian, K.; Nagura, N.; Elovic, A.;
Am. J. Pathol. 143, 130-142, 1993
A:Title: Sequential expression of transforming growth factors alpha and beta 1 by eosino-
A:Reference number: 148196; MUID:93304479; PMID:8317544
A:Accession: 148196
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-130 <RES>
A:Cross-references: UNIPROT:Q08714; EMBL:X60296; NID:G396177; PID:CAA42838.1; PID:G3961
C:Superfamily: inhibin

Query Match
Best Local Similarity 100.0%; Score 145; DB 2; Length 130;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HEPKGYHANFCLGCPYIWSLDT 23
DB 52 HEPKGYHANFCLGCPYIWSLDT 74

RESULT 2
A40057
transforming growth factor beta-1 precursor - bovine (fragment)
N:Alternate names: beta-RGF; cartilage-inducing factor-A; EGF-dependent TGF or deGF; MGF
C:Species: Bos primigenius taurus (cattle)
C:Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 09-Jul-2004
C:Accession: A40057; A42320; A42320; A24322; B61439
R:Van Ooberghen-Schilling, B.; Kondalish, P.; Ludwig, R.L.; Sporn, M.B.; Baker, C.C.
Mol. Endocrinol. 1, 693-698, 1987
A:Title: Complementary deoxyribonucleic acid cloning of bovine transforming growth facto
A:Reference number: A40057; MUID:91042552; PMID:3153459
A:Accession: A40057
A:Molecule type: mRNA
A:Residues: 1-315 <VAN>
A:Cross-references: UNIPROT:P18341; GB:M36271; NID:G163747; PID:AAA30778.1; PID:G163748
R:Ogawa, Y.; Schmidt, D.K.; Daech, J.R.; Chang, R.J.; Glaeser, C.B.
J. Biol. Chem. 267, 2325-2328, 1992
A:Title: Purification and characterization of transforming growth factor-beta2.3 and -be
A:Reference number: A42320; MUID:92129307; PMID:1733936
A:Accession: A42320
A:Molecule type: protein
A:Residues: 204-209, 'X', 211-217 <OGA>
R:Roberts, A.B.; Anzano, M.A.; Meyers, C.A.; Wideman, J.; Blacher, R.; Pan, Y.C.E.; Stei
Biochemistry 22, 5692-5698, 1983
A:Title: Purification and properties of a type beta transforming growth factor from bovi
A:Reference number: A05284; MUID:84104793; PMID:6607069

```

A;Accession: A05284
A;Molecule type: protein
A;Residues: 204-218 <ROB>
R;Sevedin, S.M.; Thompson, A.Y.; Bentz, H.; Rosen, D.M.; McPherson, J.M.; Conti, A.; Sie
A;Biol. Chem. 261, 5693-5695, 1986
A;Title: Carriage-inducing factor-A. Apparent identity to transforming growth factor-b
A;Reference number: A24322; MUID:86195954; PMID:3754555
A;Accession: A24322
A;Molecule type: protein
A;Residues: 204-233 <SEY>
R;Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.
J. Protein Chem. 10, 565-575, 1991
A;Title: Separation, purification, and sequence identification of TGF-beta1 and TGF-beta
A;Reference number: A61439; MUID:92189724; PMID:1799413
A;Accession: B61439
A;Molecule type: protein
A;Residues: 204-209, 'X', '211-217', 'XX', '220-232' <JIN>
C;Comment: This polypeptide is composed of two polypeptide chains cross-linked by disulf
C;Comment: Type II TGF does not bind to the EGF receptor and lacks intrinsic mitogenic a
ion. Cells grown in monolayer do not respond in a similar manner to these growth factors
C;Superfamily: Inhibin
C;Keywords: glycoprotein; growth factor; heterodimer
F;204-315/Product: transforming growth factor beta-1 #status experimental <MAT>
F;7,61,101/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 100.0%; Score 145; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 8,7e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HEPKGYHANFCLGCPPIWISLDT 23
Db 237 HEPKGYHANFCLGCPPIWISLDT 259

RESULT 3
WPM22
transforming growth factor beta-1 precursor [validated] - human
N;Alternate names: growth-inhibitory factor; TGF type 2; TGF-beta
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1986 #sequence revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: A27513; A01395; A22290; I59664; S53444
R;Derynck, R.; Rhee, L.; Chen, E.Y.; Van Tilburg, A.
Nucleic Acids Res. 15, 3188-3189, 1987
A;Title: Intron-exon structure of the human transforming growth factor-beta precursor g
A;Reference number: A27513; MUID:87174845; PMID:3470709
A;Accession: A27513
A;Molecule type: DNA
A;Residues: 1-390 <DER>
A;Cross-references: UNIPROT:P01137; GB:X05839; GB:Y00112; NID:G37097; PID:CAA29283.1; F
R;Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Eaton, D.H.; Bell, J.R.; Assoian, R.K.; Robert
Nature 316, 701-705, 1985
A;Title: Human transforming growth factor-beta complementary DNA sequence and expression
A;Reference number: A01395; MUID:85296501; PMID:3861940
A;Accession: A01395
A;Molecule type: mRNA
A;Residues: 1-9, 'P', '11-24', 'P', '26-159', 'R', '160-390' <DER>
A;Cross-references: GB:X02812; GB:J05114; NID:G37092; PID:CAA26580.1; PID:G37093
A;Note: the authors suggest that residues 8-23 could represent the hydrophobic core of a
R;Massague, J.; Ilike, B.
J. Biol. Chem. 260, 2636-2645, 1985
A;Title: Cellular receptors for type beta transforming growth factor. Ligand binding and
A;Reference number: A22290; MUID:85131019; PMID:2982829
A;Accession: A22290
A;Molecule type: protein
A;Residues: 279-295, 'XX', '298-301' <MAS>
R;Urnishizaki, Y.; Nishibu, Y.; Terui, T.; Koshida, Y.; Mahara, K.; Kohgo, Y.; Urushizaki,
Tumor Res. 22, 41-55, 1987
A;Title: Cloning and expression of the gene for human transforming growth factor-beta in
A;Reference number: I59664
A;Accession: I59664
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 279-390 <RES>

```

```

A;Cross-references: GB:M38449; NID:G339557; PID:AAA36735.1; PID:G339558
R;Stam, K.; Stewart, A.A.; Qu, G.Y.; Iwata, K.K.; Fenyo, D.; Chait, B.T.; Marshak, D.R.,
Biochem. J. 305, 87-92, 1995
A;Title: Physical and biological characterization of a growth-inhibitory activity purified
A;Reference number: S53444; MUID:95126934; PMID:7826358
A;Accession: S53444
A;Status: preliminary
A;Molecule type: protein
A;Residues: 279-297 <STA>
C;Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide
C;Genetics:
A;Gene: GDB:TGFB1, TGFB
A;Cross-references: GDB:120729; OMIM:190180
A;Map position: 19q13.2-19q13.2
C;Superfamily: Inhibin
C;Keywords: glycoprotein; growth factor; homodimer; mitogen; transformation
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-278/Domain: propeptide #status predicted <PRO>
F;244-246/Region: cell attachment (R-G-D) motif
F;279-390/Product: transforming growth factor beta-1 #status experimental <MAT>
F;82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 100.0%; Score 145; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HEPKGYHANFCLGCPPIWISLDT 23
Db 312 HEPKGYHANFCLGCPPIWISLDT 334

RESULT 4
WPM22
transforming growth factor beta-1 precursor - mouse
N;Alternate names: TGF type 2; TGF-beta
C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: A01396
R;Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Goeddel, D.V.
J. Biol. Chem. 261, 4377-4379, 1986
A;Title: The murine transforming growth factor-beta precursor.
A;Reference number: A01396; MUID:86168129; PMID:3007454
A;Accession: A01396
A;Molecule type: mRNA
A;Residues: 1-390 <DER>
A;Cross-references: UNIPROT:P04202; GB:M13177; NID:G201952; PID:AAA40423.1; PID:G201953
A;Note: the authors suggest that residues 8-23 could represent the hydrophobic core of a
C;Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide
C;Superfamily: Inhibin
C;Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen; transform
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-278/Domain: propeptide #status predicted <PRO>
F;244-246/Region: cell attachment (R-G-D) motif
F;279-390/Product: transforming growth factor beta-1 #status experimental <MAT>
F;82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 100.0%; Score 145; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HEPKGYHANFCLGCPPIWISLDT 23
Db 312 HEPKGYHANFCLGCPPIWISLDT 334

RESULT 5
A26960
transforming growth factor beta-1 precursor - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 05-Oct-1988 #sequence revision 05-Oct-1988 #text_change 09-Jul-2004
C;Accession: A26960
R;Sharples, K.; Plowman, G.D.; Rose, T.M.; Twardzik, D.R.; Purchio, A.F.
DNA 6, 239-244, 1987

```

A:Title: Cloning and sequence analysis of simian transforming growth factor-beta cDNA.
 A:Reference number: A26960; MUID:87246074; PMID:3474130
 A:Accession: A26960
 A:Molecule type: mRNA
 A:Residues: 1-390 <SHA>
 A:Cross-references: UNIPROT:P09533; GB:M16658; NID:g176552; PIDN:AAA55369.1; PID:g176553
 C:Superfamily: Inhibin
 C:Keywords: growth factor
 F:1.16/Domin: signal sequence
 F:1.7-390/Product: transforming growth factor beta #status predicted <SIG>

Query Match 100.0%; Score 145; DB 2; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPPIYWSLDT 23
 DB 312 HEPKGYHANFCLGCPPIYWSLDT 334

RESULT 6

transforming growth factor beta-1 - dog
 C:Species: Canis lupus familiaris (dog)
 C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 09-Jul-2004
 C:Accession: J04023
 R:Manning, A.M.; Auchampach, J.A.; Drong, R.F.; Slightom, J.L.
 Gene 155, 307-308, 1995

A:Title: Cloning of a canine cDNA homologous to the human transforming growth factor-beta
 A:Reference number: J04023; MUID:95237630; PMID:7721110
 A:Accession: J04023
 A:Molecule type: mRNA

A:Residues: 1-390 <MAN>

A:Cross-references: UNIPROT:P54831; GB:L34956; NID:g516071; PIDN:AAA51458.1; PID:g516072
 C:Comment: This factor plays a multifunctional role as a regulator of mammalian cell gro

C:Genetics:
 A:Gene: tgf-beta1
 C:Superfamily: inhibin
 C:Keywords: growth factor; transforming protein

F:288-390/Product: transforming growth factor beta 1 #status predicted <MAT>

Query Match 100.0%; Score 145; DB 2; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPPIYWSLDT 23
 DB 312 HEPKGYHANFCLGCPPIYWSLDT 334

RESULT 7

A27512
 transforming growth factor beta-1 precursor - pig
 N:Alternate names: TGF-beta

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 09-Jul-2004

C:Accession: A27512; A26356; I46657

R:Derynck, R.; Rhee, L.

Nucleic Acids Res. 15, 3187, 1987

A:Title: Sequence of the porcine transforming growth factor-beta precursor.

A:Reference number: A27512; MUID:87174844; PMID:3470708

A:Accession: A27512

A:Molecule type: mRNA

A:Residues: 1-390 <DER>

A:Cross-references: UNIPROT:P07200

R:Chelifetz, S.; Weatherbee, J.A.; Tsang, M.L.S.; Anderson, J.K.; Mole, J.E.; Lucas, R.;

Cell 48, 409-415, 1987

A:Title: The transforming growth factor-beta system, a complex pattern of cross-reactive

A:Accession: A26356

A:Molecule type: protein

A:Residues: 279-322 <CHE>

R:Kondalath, P.; Van Obberghen-Schilling, E.; Ludwig, R.L.; Dhar, R.; Sporn, M.B.; Robert

J. Biol. Chem. 263, 18333-18337, 1988

A:Title: cDNA cloning of porcine transforming growth factor-beta 1 mRNAs. Evidence for a

A:Reference number: I46657; MUID:89054010; PMID:2461367

A:Accession: I46657

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-390 <KON>

A:Cross-references: GB:M23703; NID:g755044; PIDN:AAA64616.1; PID:g755045

C:Genetics:

A:Gene: TGF-beta-1

C:Superfamily: inhibin

C:Keywords: growth factor

Query Match 100.0%; Score 145; DB 2; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPPIYWSLDT 23
 DB 312 HEPKGYHANFCLGCPPIYWSLDT 334

RESULT 8

transforming growth factor beta-1 - sheep
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004

C:Accession: I46463; S45115

R:Woodall, C.J.; McLaren, L.J.; Watt, N.J.

Gene 150, 371-373, 1994

A:Title: Sequence and chromosomal localisation of the gene encoding ovine latent transfo

A:Reference number: I46463; MUID:95121932; PMID:7821809

A:Accession: I46463

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-390 <WOO>

A:Cross-references: UNIPROT:P50414; EMBL:X76916; NID:g496648; PIDN:CAA54242.1; PID:g49666

A>Note: submitted to the EMBL Data Library, December 1993

C:Superfamily: inhibin

Query Match 100.0%; Score 145; DB 2; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPPIYWSLDT 23
 DB 312 HEPKGYHANFCLGCPPIYWSLDT 334

RESULT 9

transforming growth factor beta-1 precursor - rat
 N:Alternate names: TGF type 2; TGF-beta

C:Species: Rattus norvegicus (Norway rat)

C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004

C:Accession: S10219; P70023; S02267

R:Qian, S.W.; Kondalath, P.; Roberts, A.B.; Sporn, M.B.

Nucleic Acids Res. 18, 3059, 1990

A:Title: cDNA cloning by PCR of rat transforming growth factor beta-1.

A:Reference number: S10219; MUID:90272425; PMID:2349108

A:Accession: S10219

A:Molecule type: mRNA

A:Residues: 1-390 <QIA>

A:Cross-references: UNIPROT:P17246; EMBL:X52498; NID:g57341; PIDN:CAA36741.1; PID:g57342

R:Okada, F.; Yamaguchi, K.; Ichihara, A.; Nakamura, T.

J. Biochem. 106, 304-310, 1989

A:Title: Purification and structural analysis of a latent form of transforming growth fac

A:Reference number: P70023; MUID:90036779; PMID:2478527

A:Accession: P70023

A:Molecule type: protein

A:Residues: 30-32, 'X', 34-38, 'Q', 40-42, 'X', 44 <OKA>

R:Okada, F.; Yamaguchi, K.; Ichihara, A.; Nakamura, T.

FEBS Lett. 242, 240-244, 1989

A>Title: One of two subunits of masking protein in latent TGF-beta is a part of pro-TGF-
A;Reference number: S02267; MUID:89121078; PMID:2914605
A;Accession: S02267
A;Molecule type: protein
A;Residues: 30-32,'X','34-38','Q','40-42','X','44 <OK>
C;Superfamily: Inhibin
C;Keywords: glycoprotein; growth factor; integrin binding
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-278/Domain: propeptide #status experimental <PRO>
F;244-246/Region: cell attachment (R-G-D) motif
F;293-390/Product: transforming growth factor beta-1 #status predicted <MAT>
F;82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 145; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 312 HEPKGYHANFCLGCPYIWSLDT 334

RESULT 10
S01413
transforming growth factor beta-1 precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: S01413
R;Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.
Nucleic Acids Res. 16, 8730, 1988
A>Title: Nucleotide sequence of chicken transforming growth factor-beta 1 (TGF-beta 1).
A;Reference number: S01413; MUID:88335639; PMID:3166520
A;Accession: S01413
A;Molecule type: DNA
A;Residues: 1-391 <JAK>
A;Cross-references: UNIPROT:P07200; EMBL:X12373; NID:963808; PIDD:CAA30933.1; PID:963808
C;Superfamily: Inhibin
C;Keywords: growth factor

Query Match 100.0%; Score 145; DB 2; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 313 HEPKGYHANFCLGCPYIWSLDT 335

RESULT 11
A41918
transforming growth factor beta-4 precursor - chicken (fragment)
N;Alternate names: TGF-beta 4
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A41918; A34941; S03110
R;Burt, D.W.; Jakowlew, S.B.
Mol. Endocrinol. 6, 989-992, 1992
A>Title: Correction: a new interpretation of a chicken transforming growth factor-beta 4
A;Reference number: A41918; MUID:92357039; PMID:1335860
A;Accession: A41918
A;Molecule type: mRNA
A;Residues: 1-373 <BUR>
A;Cross-references: UNIPROT:P09531; GB:M31160; GB:X08012; GB:S41706; NID:91262437; PIDD:
A;Note: sequence extracted from NCBI backbone (NCBI:110106, NCBI:P:110187)
A;Note: this report corrects and reinterprets the sequence from reference A34941
R;Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.
Mol. Endocrinol. 2, 1186-1195, 1988
A>Title: Complementary deoxyribonucleic acid cloning of a messenger ribonucleic acid end
A;Reference number: A34941; MUID:89112198; PMID:2464131
A;Accession: A34941
A;Molecule type: mRNA
A;Residues: 'MDPMISGPGSCGSGWRPPTGTPMWSIGRRATASSCSSTSSRVRAEVGGRAL',122-209,'D',211-373 <
A;Cross-references: EMBL:X08012

A;Note: this sequence has been corrected in A41918
C;Superfamily: Inhibin
C;Keywords: glycoprotein; growth factor
F;1/Domain: signal sequence (fragment) #status predicted <SIG>
F;223-225/Region: cell attachment (R-G-D) motif
F;260-373/Product: transforming growth factor beta-4 #status predicted <MAT>
F;54,109,153/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.3%; Score 128; DB 2; Length 373;
Best Local Similarity 87.0%; Pred. No. 2.4e-10;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 295 HEPKGYHANFCLGCPYIWSLDT 317

RESULT 12
A39489
transforming growth factor beta-2 precursor - chicken
N;Alternate names: TGF-beta2
C;Species: Gallus gallus (chicken)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: A39489; A61018; S25849
R;Burt, D.W.; Paton, I.R.
DNA Cell Biol. 10, 723-734, 1991
A>Title: Molecular cloning and primary structure of the chicken transforming growth factor
A;Reference number: A39489; MUID:92075163; PMID:1683775
A;Accession: A39489
A;Molecule type: DNA
A;Residues: 1-412 <BUR>
A;Cross-references: UNIPROT:P30373; GB:X58071; NID:963810; PIDD:CAA1101.1; PID:9833616;
R;Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.
Growth Factors 2, 123-133, 1990
A>Title: Complementary deoxyribonucleic acid cloning of an mRNA encoding transforming gr
A;Reference number: A61018; MUID:90253805; PMID:2340183
A;Accession: A61018
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-94,'G','96-244','L',246-412 <JAK>
C;Genetics:
A;Introns: 115/1, 169/3, 214/1, 251/1, 309/2, 360/3
C;Superfamily: Inhibin
C;Keywords: growth factor; growth regulation; mitogen; transformation
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-300/Domain: propeptide #status predicted <PRO>
F;301-412/Product: transforming growth factor beta-2 #status predicted <MAT>

Query Match 85.5%; Score 124; DB 2; Length 412;
Best Local Similarity 82.6%; Pred. No. 9.3e-10;
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 334 HEPKGYHANFCLGCPYIWSLDT 356

RESULT 13
B61036
transforming growth factor beta-5 precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: A34929; B61036
R;Kondratieva, P.; Sande, M.J.; Smith, J.M.; Fielde, A.; Roberts, A.B.; Sporn, M.B.; Mellon,
J. Biol. Chem. 265, 1089-1093, 1990
A>Title: Identification of a novel transforming growth factor-beta (TGF-beta5) mRNA in X
A;Reference number: A34929; MUID:90110090; PMID:2295601
A;Accession: A34929
A;Molecule type: mRNA
A;Residues: 1-382 <KON>
A;Cross-references: UNIPROT:P16176; GB:J05180; NID:9214821; PIDD:AAA49968.1; PID:9214822
R;Roberts, A.B.; Rose, F.; Roche, N.S.; Colligan, J.E.; Garfield, M.; Rebbert, M.L.; Kondr
Growth Factors 2, 135-147, 1990

A/Title: Isolation and characterization of TGF-beta2 and TGF-beta5 from medium conditioned
A/Reference number: A61036; MUID:90253806; PMID:2340184
A/Accession: B61036
A/Molecule type: protein
A/Residues: 271-276, 'X', 278-284, 'XX', 287-299 <ROB>
C/Superfamily: inhibin
C/Keywords: growth factor
F/271-382/Product: transforming growth factor beta-5 #status experimental <MAT>

Query Match 84.8%; Score 123; DB 2; Length 382;
Best Local Similarity 82.6%; Pred. No. 1.2e-09;
Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HEPKGYANFCLGCPYIWSLDT 23
DB 304 HEPKGYANFCLGNCPIYIWSMDT 326

RESULT 14
A61439
transforming growth factor beta-2 - bovine
N/Alternate names: cartilage-inducing factor B; MGF-a; milk growth factor a
C/Species: Bos primigenius taurus (cattle)
C/Date: 07-Oct-1994 #sequence revision 07-Oct-1994 #text_change 09-Jul-2004
C/Accession: A61439; A25485; B42320; S15389
R/Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.
J/Title: Separation, purification, and sequence identification of TGF-beta1 and TGF-beta
A/Reference number: A61439; MUID:92189724; PMID:1799413
A/Accession: A61439
A/Molecule type: protein
A/Residues: 1-112 <JIN>
A/Cross-references: UNIPROT:P21214
A/Experimental source: milk
R/Seyedin, S.M.; Segarini, P.R.; Rosen, D.M.; Thompson, A.Y.; Bentz, H.; Graycar, J.
J. Biol. Chem. 262, 1946-1949, 1987
A/Title: Cartilage-inducing factor-B is a unique protein structurally and functionally
A/Reference number: A25485; MUID:87137406; PMID:3469199
A/Accession: A25485
A/Molecule type: protein
A/Residues: 1-30 <SEY>
A/Experimental source: bone
R/Ogawa, Y.; Schmidt, D.K.; Dasch, J.R.; Chang, R.U.; Glaser, C.B.
J. Biol. Chem. 267, 2325-2328, 1992
A/Title: Purification and characterization of transforming growth factor-beta2.3 and -be
A/Reference number: A42320; MUID:92129307; PMID:1733936
A/Accession: B42320
A/Molecule type: protein
A/Residues: 1-6, 'X', 8-14, 'XX', 17-34 <OGA>
A/Experimental source: bone
R/Cox, D.A.; Buerk, R.R.
Eur. J. Biochem. 197, 353-358, 1991
A/Title: Isolation and characterization of milk growth factor, a transforming-growth-fac
A/Reference number: S15389; MUID:91224126; PMID:2026157
A/Accession: S15389
A/Molecule type: protein
A/Residues: 1-16, 'XX', 19 <COX>
A/Experimental source: milk
C/Superfamily: inhibin
C/Keywords: growth factor; growth regulation; heterodimer; homodimer

Query Match 80.7%; Score 117; DB 2; Length 112;
Best Local Similarity 78.3%; Pred. No. 2.7e-09;
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 HEPKGYANFCLGCPYIWSLDT 23
DB 34 HEPKGYANFCLGACPIYIWSMDT 56

RESULT 15
WPXLB2
transforming growth factor beta-2 precursor - African clawed frog

C/Species: Xenopus laevis (African clawed frog)
C/Date: 12-Feb-1993 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C/Accession: S09510; A61036
R/Rebert, M.L.; Bhattacharya, N.; David, I.B.
Nucleic Acids Res. 18, 2185, 1990
A/Title: The sequence of TGF-beta2 from Xenopus laevis.
A/Reference number: S09510; MUID:90245678; PMID:2336403
A/Accession: S09510
A/Molecule type: mRNA
A/Residues: 1-413 <REB>
A/Cross-references: UNIPROT:P17247; EMBL:X51817; NID:9414789; PIDN:CA36116.1; PID:96513
R/Roberts, A.B.; Rosa, F.; Roche, N.S.; Colligan, J.E.; Garfield, M.; Rebert, M.L.; Kond
Growth Factors 2, 135-147, 1990
A/Title: Isolation and characterization of TGF-beta2 and TGF-beta5 from medium condition
A/Reference number: A61036; MUID:90253806; PMID:2340184
A/Accession: A61036
A/Molecule type: protein
A/Residues: 302-307, 'X', 309-315, 'XX', 318-319 <ROB>
C/Superfamily: inhibin
C/Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-301/Domain: propeptide #status predicted <PRO>
F/302-413/Product: transforming growth factor beta-2 #status predicted <MAT>
F/72,140,241/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 80.7%; Score 117; DB 1; Length 413;
Best Local Similarity 78.3%; Pred. No. 8.8e-09;
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 HEPKGYANFCLGCPYIWSLDT 23
DB 335 HEPKGYANFCLGACPIYIWSMDT 357

Search completed: June 14, 2005, 15:52:10
Job time : 25.6538 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: June 14, 2005, 15:34:23 ; Search time 122.962 Seconds

(without alignments)
95.785 Million cell updates/sec

Title: US-09-831-253F-10
Perfect score: 145
Sequence: 1 HEPKGYHANFCLGPCPYMSLDT 23

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:.*
1: uniprot_sprotc:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	145	100.0	50 2 Q28240	Q28240 cervus elap
2	145	100.0	51 2 Q72487	Q72487 homo sapien
3	145	100.0	78 2 Q70316	Q70316 sus scrofa
4	145	100.0	112 2 Q02730	Q02730 oryctolagus
5	145	100.0	124 2 Q95N80	Q95N80 canis famli
6	145	100.0	130 2 Q08714	Q08714 mesocricetu
7	145	100.0	315 1 TGFI BOVIN	P18341 bos taurus
8	145	100.0	368 2 Q8R4D9	Q8R4D9 sigmodon hi
9	145	100.0	390 1 TGFI CANRA	P54831 canis famli
10	145	100.0	390 1 TGFI CAURO	Q921Y6 cavia porce
11	145	100.0	390 1 TGFI CERAE	P09533 cercopithec
12	145	100.0	390 1 TGFI HORSE	O19011 equus cabal
13	145	100.0	390 1 TGFI HUMAN	P01137 homo sapien
14	145	100.0	390 1 TGFI MOUSE	P04202 mus musculu
15	145	100.0	390 1 TGFI PIG	P07200 sus scrofa
16	145	100.0	390 1 TGFI RAT	P17246 rattus norv
17	145	100.0	390 1 TGFI SHEEP	P50414 ovib aries
18	145	100.0	390 2 Q9TUM6	Q9TUM6 equus cabal
19	138	95.2	101 2 Q9R184	Q9R184 meriones un
20	128	88.3	373 1 TGFI CHICK	P09531 gallus galli
21	124	85.5	412 1 TGFI CHICK	P30371 gallus galli
22	123	84.8	382 1 TGFI XENLA	P16176 xenopus lae
23	118	81.4	77 2 Q90YF8	Q90YF8 oncorhynch
24	118	81.4	88 2 Q90YF7	Q90YF7 oncorhynch
25	118	81.4	91 2 Q9MYZ1	Q9MYZ1 capra hircu
26	118	81.4	361 2 Q98854	Q98854 cyprinus ca
27	118	81.4	410 2 Q66123	Q66123 brachydanio
28	118	81.4	410 2 Q7SZV3	Q7SZV3 brachydanio
29	118	81.4	411 2 Q90YF4	Q90YF4 pleuronecte
30	117	80.7	62 2 Q90YF4	Q90YF4 pleuronecte
31	117	80.7	86 2 Q28241	Q28241 cervus elap

32	117	80.7	112 1 TGFI BOVIN	P21214 bos taurus
33	117	80.7	224 2 Q8CDZ9	Q8CDZ9 mus musculu
34	117	80.7	255 2 Q921T1	Q921T1 mus musculu
35	117	80.7	399 2 Q9ERB7	Q9ERB7 mesocricetu
36	117	80.7	413 1 TGFI XENLA	P17247 xenopus lae
37	117	80.7	414 1 TGFI CERAE	P61811 cercopithec
38	117	80.7	414 1 TGFI HUMAN	P61812 homo sapien
39	117	80.7	414 1 TGFI MOUSE	P27090 mus musculu
40	117	80.7	414 2 Q91VP5	Q91VP5 mus musculu
41	117	80.7	435 1 TGFI PIG	P09856 sus scrofa
42	117	80.7	442 1 TGFI RAT	Q07257 rattus norv
43	117	80.7	442 2 Q6TFC3	Q6TFC3 oryctolagus
44	112	77.2	62 2 Q90YF9	Q90YF9 oncorhynch
45	112	77.2	62 2 Q90ZJ8	Q90ZJ8 anguilla an

ALIGNMENTS

```

RESULT 1
Q28240 PRELIMINARY; PRT; 50 AA.
ID Q28240
AC Q28240
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Transforming growth factor beta 1 (TGF-beta 1) (Transforming growth
DE factor B1) (Fragment).
GN Name=TGFB1; Synonyms=TGF beta-1, TGF-B1;
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervinae; Cervus.
OX NCBI_TaxID=96860;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Antler;
RX MEDLINE=98233260; PubMed=9571767;
RA DOI=10.1002/(SICI)1097-010X(19980501)281:1<36::AID-JEZ6>3.0.CO;2-D;
RA Francis S.M., Suttie J.M.;
RT "Detection of growth factors and proto-oncogene mRNA in the growing
RT tip of red deer (Cervus elaphus) antler using reverse-transcriptase
RT polymerase chain reaction (RT-PCR).";
RL J. Exp. Zool. 281:36-42(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Wagener A., Bloctner S., Fickel J.;
RT "Detection of growth factors in the testes of roe deer (Capreolus
RT capreolus).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
CC THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
CC REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
CC DERIVATIVES. A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -I- SUBUNIT: Homodimer; disulfide-linked (by similarity).
CC -I- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; U62110; AAB05256.1; -.
DR EMBL; AF152591; AAF73230.1; -.
DR HSSP; P01137; IKLA.
DR GO; GO:0008083; P:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000704; P:regulation of cell cycle; IEA.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SMO0204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Glycoprotein; Growth Factor; Mitogen.
FT NON_TER
FT CHAIN <1 >50 TRANSFORMING GROWTH FACTOR BETA 1.

```

[illegible]

DR	GO; GO:0080083; F:growth factor activity; IEA.
DR	InterPro; IPR001839; TGFb.
DR	Pfam; PF00019; TGF_beta; 1.
DR	ProDom; PD000357; TGFb; 1.
DR	SMART; SM00204; TGFb; 1.
KW	PROSITE; PS00250; TGF_BETA_1; 1.
DR	Growth factor.
FT	NON TER 1 1
FT	CHAIN <1 >78
FT	NON TER 78 78
SQ	SEQUENCE 78 AA; 8981 MW; 1BAI79E147738152 CRC64;
Query Match	
Best Local Similarity	100.0%; Score 145; DB 2; Length 78;
Matches	23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 HEPKGYANFCLGPCPYIMSLDT 23
Dd	18 HEPKGYANFCLGPCPYIMSLDT 40
RESULT 4	
ID	002730 PRELIMINARY; PRT; 112 AA.
AC	002730; O97501;
DT	01-JUL-1997 (TREMBLrel. 04; Created)
DT	01-JUL-1997 (TREMBLrel. 04; Last sequence update)
DE	01-MAR-2004 (TREMBLrel. 26; Last annotation update)
DE	Transforming growth factor beta 1 (TGF-beta 1) (Fragment).
GN	Name=TGFBI; Synonyms=TGF-beta-1;
OS	Oryctolagus cuniculus (Rabbit).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI	NCBI_TaxId=9986;
RN	[1]
RA	SEQUENCE FROM N.A.
RL	Taylor T.K., James E.R., McGonigle S., Yoho E.R.; Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
RN	(2)
RA	SEQUENCE OF 2-99 FROM N.A.
RL	Inoue K., Kawabe Y., Kodama T.; Submitted (Nov-1998) to the EMBL/GenBank/DBJ databases.
CC	- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS. - SUBUNIT: Homodimer; disulfide-linked (By similarity). - SIMILARITY: Belongs to the TGF-beta family.
CC	EMBL; AF000133; AAB53806.1; -
DR	EMBL; AB020217; BAA36950.1; -
DR	HSSP; P01137; IKLA.
DR	GO; GO:0008083; F:growth factor activity; IEA.
DR	GO; GO:0008283; P:cell proliferation; IEA.
DR	GO; GO:000074; P:regulation of cell cycle; IEA.
DR	InterPro; IPR002400; GF_cyknot.
DR	InterPro; IPR001839; TGFb.
DR	Pfam; PF00019; TGF_beta; 1.
DR	PRINTS; PR00438; GFCYSKNOT.
DR	ProDom; PD000357; TGFb; 1.
DR	SMART; SM00204; TGFb; 1.
DR	PROSITE; PS00250; TGF_BETA_1; 1.
KW	GLYCOPROTEIN; Growth Factor; Mitogen.
FT	NON TER 1 1
FT	CHAIN 1 112
FT	DISULFID 7 16
FT	DISULFID 15 78
FT	DISULFID 44 109
FT	DISULFID 48 111
FT	DISULFID 77 77
FT	CONFLICT 2 3
FT	CONFLICT 85 92
FT	CONFLICT ID -> FS (IN REF. 2).
FT	CONFLICT PLPIYIV -> ATAHRTITL (IN REF. 2).
FT	CONFLICT TRANSFORMING GROWTH FACTOR BETA 1.
FT	CONFLICT BY SIMILARITY.
FT	CONFLICT BY SIMILARITY.
FT	CONFLICT BY SIMILARITY.
FT	CONFLICT INTERCHAIN (BY SIMILARITY).
FT	CONFLICT ID -> FS (IN REF. 2).
FT	CONFLICT PLPIYIV -> ATAHRTITL (IN REF. 2).

SQ SEQUENCE 112 AA; 12795 MW; 53C5B7D46355A6F3 CRC64;
 Query Match 100.0%; Score 145; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 3.2e-13;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HEPKGYHANFCLGCPYIWSLDT 23
 |||||
 DB 34 HEPKGYHANFCLGCPYIWSLDT 56
 |||||
 RESULT 5
 Q95N80 PRELIMINARY; PRT; 124 AA.
 AC Q95N80;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DE Transforming growth factor beta 1 (Fragment).
 OS Canis familiaris (dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pontara S., Groene A., Baumgaertner W.;
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 DR EMBL; AF349538; AAK54072.1; -.
 DR HSSP; P01137; IKLA.
 DR GO; GO:0008083; F:growth factor activity; IEA.
 DR InterPro; IPR001839; TGFb.
 DR Pfam; PF00018; TGF_beta.1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KM Growth factor.
 FT NON_TER 1 1
 FT NON_TER 124 124
 SQ SEQUENCE 124 AA; 14329 MW; 21D185218E5556DB CRC64;
 Query Match 100.0%; Score 145; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 3.5e-13;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HEPKGYHANFCLGCPYIWSLDT 23
 |||||
 DB 49 HEPKGYHANFCLGCPYIWSLDT 71
 |||||
 RESULT 6
 Q08714 PRELIMINARY; PRT; 130 AA.
 ID Q08714; 070331;
 AC Q08714; 070331;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DE Transforming growth factor beta 1 (TGF-beta 1) (Fragment).
 GN Name=TGFb1;
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LVG (SVR);
 RA MEDLINE=93304479; PubMed=8317544;
 RA Wong D.T., Donoff R.B., Yang J., Song B.Z., Matossian K., Nagura N.,
 RA Elvolic A., McBride J., Gallagher G., Todd R.;
 RT "Sequential expression of transforming growth factors alpha and beta 1
 RT by eosinophils during cutaneous wound healing in the hamster.";
 RL Am. J. Pathol. 143:130-142(1993).

RN [2]
 RP SEQUENCE OF 26-115 FROM N.A.
 RC STRAIN=SYRIAN; TISSUE=SPLEEN;
 RX MEDLINE=98234044; PubMed=9573100;
 RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
 RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
 RT leishmaniasis.";
 RT Infect. Immun. 66:2135-2142(1998).
 RL -1- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
 CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
 CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
 CC THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
 CC REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
 CC DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
 CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
 DR EMBL; X60296; CAA42838.1; -.
 DR EMBL; AF046214; AAC40099.1; -.
 DR PIR; I48196; I48196.
 DR HSSP; P01137; IKLA.
 DR GO; GO:0008083; F:growth factor activity; IEA.
 DR GO; GO:0008283; P:cell proliferation; IEA.
 DR GO; GO:0000704; P:regulation of cell cycle; IEA.
 DR InterPro; IPR001839; TGFb.
 DR Pfam; PF00019; TGF_beta; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 DR Glycoprotein; Growth factor; Mitogen.
 FT NON_TER 1 1
 FT PRODP <1 18
 FT CHAIN 25 130
 FT DISULFD 25 34 BY SIMILARITY.
 FT DISULFD 33 96 BY SIMILARITY.
 FT DISULFD 66 129 BY SIMILARITY.
 FT DISULFD 95 95 INTERCHAIN (BY SIMILARITY).
 FT CONFLICT 93 93 G->S (IN REF. 2).
 SQ SEQUENCE 130 AA; 14997 MW; 8B41D6C39CCA77 CRC64;
 Query Match 100.0%; Score 145; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 3.6e-13;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HEPKGYHANFCLGCPYIWSLDT 23
 |||||
 DB 52 HEPKGYHANFCLGCPYIWSLDT 74
 |||||
 RESULT 7
 TGF1_BOVIN STANDARD; PRT; 315 AA.
 ID TGF1_BOVIN
 AC P18341;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1) (Fragment).
 GN Name=TGFb1;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=91042552; PubMed=3153459;
 RA van Obberghen-Schilling E., Kondalish P., Ludwig R.L., Sporn M.B.,
 RA Baker C.C.;
 RT "Complementary deoxyribonucleic acid cloning of bovine transforming
 RT growth factor-beta 1.";
 RL Mol. Endocrinol. 1:693-698(1987).
 RN [2]
 RP SUBUNITS.

CC TISSUE=Bone; PubMed=1733936;
RX MEDLINE=92129307; Daesch J.R., Chang R.J., Glaser C.B.;
RA Ogawa Y., Schmidt D.K., Daesch J.R., Chang R.J., Glaser C.B.;
RT "Purification and characterization of transforming growth factor-beta
2.3 and -beta 1.2 heterodimers from bovine bone.";
RL J. Biol. Chem. 267:2325-2328 (1992).
CC -1- FUNCTION: TGF-beta is a multifunctional peptide that controls
proliferation, differentiation, and other functions in many cell
types. Many cells synthesize TGF-beta and essentially all of them
have specific receptors for this peptide. TGF-beta regulates the
actions of many other peptide growth factors and determines a
positive or negative direction of their effects. Play an important
role in bone remodeling. It is a potent stimulator of
osteoblastic bone formation, causing chemotaxis, proliferation and
differentiation in committed osteoblasts (By similarity).
CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
covalently linked to a latency-associated peptide (LAP) homodimer.
The inactive complex can contain a latent TGF-beta binding protein
(By similarity). The active form is a homodimer of mature TGF-beta
1; disulfide-linked. Heterodimers of TGF-beta 1/2 have been found
in bone.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1
and LAP (By similarity).
CC -1- SIMILARITY: Belongs to the TGF-beta family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR EMBL, M36271; AAA30778.1; -.
DR PIR, A40057; A40057.
DR HSSP, P01137; IKLA.
DR InterPro: IPR002400; GF_cyknoc.
DR InterPro: IPR003911; TGF_TGFB.
DR InterPro: IPR001839; TGFB.
DR InterPro: IPR001111; TGFB_N.
DR Pfam, PF00019; TGF_beta_1.
DR PRINTS; PR00688; TGFB_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD000357; TGFB; 1.
DR SMART; SM00204; TGFB; 1.
DR PROSITE; PS00250; TGF_beta_1; 1.
KW Glycoprotein; Growth factor; Mitogen.
FT NON_TER 1
FT PROPEP 1
FT CHAIN 204 315 Transforming growth factor beta 1.
FT DISULFD 210 219 By similarity.
FT DISULFD 218 281 By similarity.
FT DISULFD 247 312 By similarity.
FT DISULFD 251 314 By similarity.
FT DISULFD 280 280 Interchain (By similarity).
FT CARBOHD 7 7 N-linked (GlcNAc...) (By similarity).
FT CARBOHD 61 61 N-linked (GlcNAc...) (By similarity).
FT CARBOHD 101 101 N-linked (GlcNAc...) (By similarity).
FT SITE 169 171 Cell attachment site (Potential).
SQ SEQUENCE 315 AA; 36269 MW; C2717A23D994800E CRC64;
Query Match 100.0%; Score 145; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 8.2e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HEPKGYHANFCLGCPYIWSLDT 23
DB 237 HEPKGYHANFCLGCPYIWSLDT 259
RESULT 8

QBRAD9 ID QBRAD9 PRELIMINARY; PRT; 368 AA.
AC QBRAD9;
DT 01-JUN-2002 (TRENBLREL. 21, Created)
DT 01-JUN-2002 (TRENBLREL. 21, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Transforming growth factor beta-1 protein (fragment).
GN Name=Tgfb1;
OS Sismodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sismodon.
OX NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14980083; DOI=10.1089/10799900477219873;
RA Blanco J.C., Plateney L., Boukhalova M., Richardson J.Y.,
Harris K.A., Prince G.A.;
RT "The cotton rat: an underutilized animal model for human infectious
diseases can now be exploited using specific reagents to cytokines,
chemokines, and interferons.";
RL J. Interferon Cytokine Res. 24:21-28(2004).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC EMBL, AF460858; AAB87199.1; -.
DR HSSP, P01137; IKLA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0005160; F:transforming growth factor beta receptor bi.; IEA.
DR GO; GO:0016049; P:cell growth; IEA.
DR InterPro: IPR002400; GF_cyknoc.
DR InterPro: IPR001839; TGFB.
DR InterPro: IPR003939; TGFB_N.
DR InterPro: IPR001111; TGFB_N.
DR InterPro: IPR003911; TGF_TGFB.
DR Pfam; PF00688; TGFB_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD000357; TGFB; 1.
DR SMART; SM00204; TGFB; 1.
DR PROSITE; PS00250; TGF_beta_1; 1.
KW Growth factor.
FT NON_TER 1
FT SEQUENCE 368 AA; 41905 MW; A5C91207B0468BA CRC64;
Query Match 100.0%; Score 145; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 9.4e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HEPKGYHANFCLGCPYIWSLDT 23
DB 290 HEPKGYHANFCLGCPYIWSLDT 312
RESULT 9
TGFI CANFA STANDARD; PRT; 390 AA.
ID TGFI CANFA
AC P54831;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN Name=TGFBI;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX Tissue=Jugular vein endothelial;
MEDLINE=95237630; PubMed=7721110; DOI=10.1016/0378-1119(94)00903-6;
Manning A.W., Auchampach J.A., Drong R.F., Slightom J.L.;
RT "Cloning of a canine cDNA homologous to the human transforming growth

RT factor-beta 1-encoding gene.;

RL Gene 155:307-308(1995).

CC -1- FUNCTION: TGF-beta is a multifunctional peptide that controls proliferation, differentiation, and other functions in many cell types. Many cells synthesize TGF-beta and essentially all of them have specific receptors for this peptide. TGF-beta regulates the actions of many other peptide growth factors and determines a positive or negative direction of their effects. Play an important role in bone remodeling. It is a potent stimulator of osteoblastic bone formation, causing chemotaxis, proliferation and differentiation in committed osteoblasts (By similarity).

CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-covalently linked to a latency-associated peptide (LAP) homodimer. The inactive complex can contain a latent TGF-beta binding protein. The active form is a homodimer of mature TGF-beta 1; disulfide-linked (By similarity).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1 and LAP (By similarity).

CC -1- SIMILARITY: Belongs to the TGF-beta family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

DR EMBL: L34956; AAA51458.1; -.

DR PIR: J04023; J04023.

DR HSSP: P01137; IKLA.

DR InterPro: IPR002400; GF_cysknot.

DR InterPro: IPR003911; TGF_TGFB.

DR InterPro: IPR001839; TGFB.

DR InterPro: IPR001111; TGFB_N.

DR Pfam: PF00019; TGF_beta; 1.

DR Pfam: PF00688; TGFB_propeptide; 1.

DR PRINTS: PR00438; GRCYSKNOT.

DR PRINTS: PR01423; TGFEBETA.

DR PRODOM: PD000357; TGFB; 1.

DR SMART: SM00204; TGFB; 1.

DR PROSITE: PS00250; TGF_BETA_1; 1.

KM Glycoprotein; Growth Factor; Mitogen; Signal.

FT SIGNAL 1 29

FT PROPEP 30 278

FT CHAIN 279 390

FT DISULFID 285 294

FT DISULFID 293 356

FT DISULFID 322 387

FT DISULFID 326 389

FT DISULFID 355 355

FT CARBOHYD 82 82

FT CARBOHYD 136 136

FT CARBOHYD 176 176

FT SITE 244 246

SQ SEQUENCE 390 AA; 44185 MW; E84780E88B7B590E CRC64;

Query Match 100.0%; Score 145; DB 1; Length 390;

Best Local Similarity 100.0%; Pred. No. 9-9e-13;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPPIYWSIDT 23

Db 312 HEPKGYHANFCLGCPPIYWSIDT 334

RESULT 10

TGFI_CAVPO STANDARD; PRT; 390 AA.

AC Q921Y6; Q9QZB3; Q9R148;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DR Transforming growth factor beta 1 precursor (TGF-beta 1).

GN Name=TGFBI;

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.

OX NCBI_TaxID=10141;

RP [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Hartley;

RA Jeevan A., McMurray D.N., Yoshimura T.;

RT "Guinea pig transforming growth factor-beta in peritoneal exudates after BCG vaccination.";

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 265-382 FROM N.A.

RX MEDLINE=99144670; PubMed=10025978; DOI=10.1016/S1043-4666(98)90002-3;

RA Scarozza A.M., Ramsingh A.I., Wicher V., Wicher K.;

RT "Spontaneous cytokine gene expression in normal guinea pig blood and tissues".;

RL Cytokine 10:851-859(1998).

RN [3]

RP SEQUENCE OF 279-371 FROM N.A.

RC STRAIN=Hartley; TISSUE=Trachea;

RA Morishima Y., Uchida Y., Nomura A., Ishii Y., Sakamoto T., Sekizawa K.;

RT "Guinea-pig transforming growth factor-beta expression in injured tracheal epithelium.";

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Multifunctional peptide that controls proliferation, differentiation, and other functions in many cell types. Many cells synthesize TGF-beta 1 and essentially all of them have specific receptors for this peptide. TGF-beta 1 regulates the actions of many other peptide growth factors and determines a positive or negative direction of their effects. Play an important role in bone remodeling. It is a potent stimulator of osteoblastic bone formation, causing chemotaxis, proliferation and differentiation in committed osteoblasts (By similarity).

CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-covalently linked to a latency-associated peptide (LAP) homodimer. The inactive complex can contain a latent TGF-beta binding protein. The active form is a homodimer of mature TGF-beta 1; disulfide-linked (By similarity).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1 and LAP (By similarity).

CC -1- SIMILARITY: Belongs to the TGF-beta family.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

DR EMBL: AF191297; AF02780.1; -.

DR EMBL: AF097509; AAC83807.1; -.

DR EMBL: AF169347; AAD49347.1; -.

DR HSSP: P01137; IKLA.

DR InterPro: IPR002400; GF_cysknot.

DR InterPro: IPR003911; TGF_TGFB.

DR InterPro: IPR001839; TGFB.

DR InterPro: IPR001111; TGFB_N.

DR Pfam: PF00019; TGF_beta; 1.

DR Pfam: PF00688; TGFB_propeptide; 1.

DR PRINTS: PR00438; GRCYSKNOT.

DR PRINTS: PR01423; TGFEBETA.

DR PRODOM: PD000357; TGFB; 1.

DR SMART: SM00204; TGFB; 1.

DR PROSITE: PS00250; TGF_BETA_1; 1.

KM Glycoprotein; Growth Factor; Mitogen; Signal.

FT SIGNAL 1 29 By similarity.
 FT PROPEP 30 278 latency-associated peptide (By
 FT CHAIN 279 390 transforming growth factor beta 1.
 FT DISULFID 285 294 By similarity.
 FT DISULFID 293 356 By similarity.
 FT DISULFID 322 387 By similarity.
 FT DISULFID 326 389 By similarity.
 FT CARBOHYD 355 355 Interchain (By similarity).
 FT CARBOHYD 82 82 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 136 136 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 176 176 N-linked (GlcNAc...) (By similarity).
 FT SITE 244 246 Cell attachment site (Potential).
 FT CONFLICT 279 279 G -> P (in Ref. 2).
 FT CONFLICT 286 286 F -> S (in Ref. 2).
 FT CONFLICT 309 309 K -> R (in Ref. 2).
 FT CONFLICT 322 322 C -> R (in Ref. 2).
 FT CONFLICT 350 350 A -> G (in Ref. 2).
 SQ SEQUENCE 390 AA; 44328 MW; 1539F849BA0C0CF1 CRC64;

Query Match 100.0%; Score 145; DB 1; Length 390;
 Best Local Similarity 100.0%; Pred. No. 9.9e-13;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HEPKGYHANFCLGCPYIWSLDT 23
 Db 312 HEPKGYHANFCLGCPYIWSLDT 334

RESULT 11
 TGF1_CERAE STANDARD; PRT; 390 AA.
 ID TGF1_CERAE STANDARD; PRT; 390 AA.
 AC P09533;
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).
 GN Name=TGFb1;
 OS Cercopithecus aethiops (Green monkey) (Primate).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 OC NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87246074; PubMed=3474130;
 RA Sharples K., Plowman G.D., Rose T.M., Twardzik D.R., Purchio A.F.,
 RT "Cloning and sequence analysis of simian transforming growth factor-
 beta cDNA.";
 RL DNA 6:239-244 (1987).
 RN [2]
 RP GLYCOSYLATION.
 RX PubMed=2971654;
 RA Purchio A.F., Cooper J.A., Brunner A.M., Lioubin M.N., Gentry L.E.,
 RA Kovachina K.S., Roth R.A., Marguardt H.;
 RT "Identification of mannose 6-phosphate in two asparagine-linked sugar
 chains of recombinant transforming growth factor-beta 1 precursor.";
 RL J. Biol. Chem. 263:14211-14215 (1988).
 RN [3]
 RP CHARACTERIZATION.
 RX PubMed=3185545;
 RA Gentry L.E., Lioubin M.N., Purchio A.F., Marguardt H.;
 RT "Molecular events in the processing of recombinant type 1 pre-pro-
 transforming growth factor beta to the mature polypeptide.";
 RL Mol. Cell. Biol. 8:4162-4168 (1988).
 CC -1- FUNCTION: Multifunctional peptide that controls proliferation,
 differentiation, and other functions in many cell types. Many
 cells synthesize TGF-beta 1 and essentially all of them have
 specific receptors for this peptide. TGF-beta 1 regulates the
 actions of many other peptide growth factors and determines a
 positive or negative direction of their effects. Plays an important
 role in bone remodelling. It is a potent stimulator of
 osteoblastic bone formation, causing chemotaxis, proliferation and

CC differentiation in committed osteoblasts (By similarity).
 CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
 CC covalently linked to a latency-associated peptide (LAP) homodimer.
 CC The inactive complex can contain a latent TGF-beta binding
 CC protein. The active form is a homodimer of mature TGF-beta 1;
 CC disulfide-linked.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1
 CC and LAP, which remains non-covalently linked to mature TGF-beta 1
 CC rendering it inactive.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).

CC EMBL/ M16658; AAA5369.1; -.
 CC PIR; A26960; A26960.
 DR HSSP; P01137; 1KLA.
 DR InterPro; IPR002400; GF_cysknot.
 DR InterPro; IPR003911; TGF_TGFB.
 DR InterPro; IPR001839; TGFB.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF000019; TGF_beta_1.
 DR Pfam; PF00688; TGFB_propeptide; 1.
 DR PRINTS; PR00438; GRCYSKNOT.
 DR PRINTS; PR01423; TGFbeta.
 DR ProDom; PD000357; TGFB_1.
 DR SMART; SM00204; TGFB; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 DR Glycoprotein; Growth Factor; Mitogen; Signal.
 KW SIGNAL 1 29
 FT PROPEP 30 278 latency-associated peptide.
 FT CHAIN 279 390 Transforming growth factor beta 1.
 FT DISULFID 285 294 By similarity.
 FT DISULFID 293 356 By similarity.
 FT DISULFID 322 387 By similarity.
 FT DISULFID 326 389 By similarity.
 FT DISULFID 355 355 Interchain (By similarity).
 FT CARBOHYD 82 82 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 136 136 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 176 176 N-linked (GlcNAc...) (By similarity).
 FT SITE 244 246 Cell attachment site (Potential).
 SQ SEQUENCE 390 AA; 44356 MW; DFF63B2BBA4320B CRC64;

Query Match 100.0%; Score 145; DB 1; Length 390;
 Best Local Similarity 100.0%; Pred. No. 9.9e-13;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HEPKGYHANFCLGCPYIWSLDT 23
 Db 312 HEPKGYHANFCLGCPYIWSLDT 334

RESULT 12
 TGF1_HORSE STANDARD; PRT; 390 AA.
 ID TGF1_HORSE STANDARD; PRT; 390 AA.
 AC O19011;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).
 GN Name=TGFb1;
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OC NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.

CC TISSUE=Lymph node;
 RX MEDLINE=98185507; PubMed=9524819;
 RA Penha-Goncalves M.N., Onions D.E., Nicolson L.;
 RT "Cloning and sequencing of equine transforming growth factor-beta 1
 (TGF-beta-1) cDNA.";
 RL DNA Seq. 7:375-378(1997).
 CC -1- FUNCTION: TGF-beta is a multifunctional peptide that control
 proliferation, differentiation, and other functions in many cell
 types. Many cells synthesize TGF-beta and essentially all of them
 have specific receptors for this peptide. TGF-beta regulates the
 actions of many other peptide growth factors and determines
 positive or negative direction of their effects. Play an important
 role in bone remodelling. It is a potent stimulator of
 osteoblastic bone formation, causing chemotaxis, proliferation and
 differentiation in committed osteoblasts (By similarity).
 CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
 covalently linked to a latency-associated peptide (LAP) homodimer.
 CC The inactive complex can contain a latent TGF-beta binding
 CC protein. The active form is a homodimer of mature TGF-beta 1;
 CC disulfide-linked (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1
 CC and LAP (By similarity).
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-ch.ch).
 CC -----
 CC EMBL; X99438; CA67801.1; -.
 DR HSSP; P01137; 1KLA.
 DR InterPro; IPR002400; GF_cyskn0t.
 DR InterPro; IPR003911; TGF_TGFB.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF_beta_1.
 DR Pfam; PF00688; TGFb_propeptide_1.
 DR PRINTS; PRO0438; GFCYSKN0T.
 DR PRINTS; PRO1423; TGFbeta.
 DR PRODOM; PD000357; TGFb_1.
 DR SMART; SM00204; TGFb_1.
 DR PROSITE; PS00250; TGF_beta_1; 1.
 KW Glycoprotein; Growth factor; Mitogen; Signal.
 FT SIGNAL 1 29 By similarity.
 FT PROPEP 30 278 Latency-associated peptide (By
 FT similarity).
 FT CHAIN 279 390 Transforming growth factor beta 1.
 FT DISULFD 285 294 By similarity.
 FT DISULFD 293 356 By similarity.
 FT DISULFD 322 387 By similarity.
 FT DISULFD 326 389 By similarity.
 FT DISULFD 355 385 Interchain (By similarity).
 FT CARBOHD 82 82 N-linked (GlcNAc...) (By similarity).
 FT CARBOHD 136 136 N-linked (GlcNAc...) (By similarity).
 FT CARBOHD 176 176 N-linked (GlcNAc...) (By similarity).
 SQ SEQUENCE 390 AA; 43974 MW; A86D715F44549691 CRC64;

Query Match 100.0%; Score 145; DB 1; Length 390;
 Best Local Similarity 100.0%; Pred. No. 9.9e-13;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HEPKGYHANFCLGRCPTIWSLDT 23
 DB 312 HEPKGYHANFCLGRCPTIWSLDT 334

RESULT 13
 TGF1_HUMAN
 ID_TGF1_HUMAN STANDARD: PRT; 390 AA.

AC P01137; Q9UCG4;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).
 GN Name=TGFb1; Synonyms=TGFb;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OK NCBI_Taxid=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87174845; PubMed=3470709;
 RA Derynck R., Rhee L., Chen E.Y., van Tilburg A.;
 RT "Intron-exon structure of the human transforming growth factor-beta
 RT precursor gene.";
 RL Nucleic Acids Res. 15:3188-3189(1987).
 RN (2)
 RP SEQUENCE FROM N.A., AND VARIANT PRO-10.
 RX MEDLINE=85296301; PubMed=3861940;
 RA Derynck R., Jarrett J.A., Chen E.Y., Eaton D.H., Bell J.R.,
 RA Asseban R.K., Roberts A.B., Sporn W.B., Goeddel D.V.;
 RT "Human transforming growth factor-beta complementary DNA sequence and
 RT expression in normal and transformed cells.";
 RL Nature 316:701-705(1985).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ductum, and Eye;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strusberg R.L., Felsing E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rahn S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalske U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (4)
 RP SEQUENCE OF 279-390 FROM N.A.
 RC TISSUE=Carcinoma;
 RA Urushizaki Y., Nitsu Y., Terui T., Koshida Y., Mahara K., Kohgo Y.,
 RA Urushizaki I., Takahashi Y., Ito H.;
 RT "Cloning and expression of the gene for human transforming growth
 RT factor-beta in Escherichia coli.";
 RL Tumor Res. 22:41-55(1987).
 RN (5)
 RP SEQUENCE OF 279-329.
 RC TISSUE=Bladder carcinoma;
 RX MEDLINE=93229900; PubMed=8471846; DOI=10.1006/prep.1993.1019;
 RA Bourdrel L., Lin C.-H., Lauren S.L., Elmore R.H., Sugarman B.J.,
 RA Hu S., Westcott K.R.;
 RT "Recombinant human transforming growth factor-beta 1: expression by
 RT Chinese hamster ovary cells, isolation, and characterization.";
 RL Protein Expr. Purif. 4:130-140(1993).
 RN (6)
 RP SEQUENCE OF 279-301.
 RX MEDLINE=85131019; PubMed=2982829;
 RA Massague J., Lile B.;
 RT "Cellular receptors for type beta transforming growth factor. Ligand
 RT binding and affinity labeling in human and rodent cell lines.";
 RL J. Biol. Chem. 260:2636-2645(1985).

[7]
 RP SEQUENCE OF 30-42 AND 279-290, AND CHARACTERIZATION.
 RX PubMed=3162913;
 RA Miyazono K., Heilman U., Wernstedt C., Heldin C.H.;
 RT "Latent high molecular weight complex of transforming growth factor
 beta 1. Purification from human platelets and structural
 characterization.";
 RL J. Biol. Chem. 263:6407-6415(1988).
 RN [8]
 RP REVIEW.
 RX PubMed=9150447;
 RA Munger J.S., Harpel J.G., Gleizes P.E., Mazziere R., Nunes I.,
 RA Rifkin D.B.;
 RT "Latent transforming growth factor-beta: structural features and
 RT mechanisms of activation.";
 RL Kidney Int. 51:1376-1382(1997).
 RN [9]
 RP STRUCTURE BY NMR OF 279-390.
 RX MEDLINE=93144319; PubMed=8424942;
 RA Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez K.A.,
 RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
 RA Torchia D.A.;
 RT "Transforming growth factor beta 1: NMR signal assignments of the
 RT recombinant protein expressed and isotopically enriched using Chinese
 RT hamster ovary cells.";
 RL Biochemistry 32:1152-1163(1993).
 RN [10]
 RP STRUCTURE BY NMR OF 279-390.
 RX MEDLINE=93144320; PubMed=8424943;
 RA Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez K.A.,
 RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
 RA Torchia D.A.;
 RT "Transforming growth factor beta 1: secondary structure as determined
 RT by heteronuclear magnetic resonance spectroscopy.";
 RL Biochemistry 32:1164-1171(1993).
 RN [11]
 RP STRUCTURE BY NMR OF 279-390.
 RX MEDLINE=96266150; PubMed=8679613; DOI=10.1021/bi9604946;
 RA Hinck A.P., Archer S.J., Qian S.W., Roberts A.B., Sporn M.B.,
 RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
 RA Torchia D.A.;
 RT "Transforming growth factor beta 1: three-dimensional structure in
 RT solution and comparison with the X-ray structure of transforming
 RT growth factor beta 2.";
 RL Biochemistry 35:8517-8534(1996).
 RN [12]
 RP TISSUE SPECIFICITY.
 RX PubMed=11746498; DOI=10.1002/jcb.1249;
 RA Shur I., Lokietz F., Bleiberg I., Benayahu D.;
 RT "Differential gene expression of cultured human osteoblasts.";
 RL J. Cell. Biochem. 83:547-553(2001).
 RN [13]
 RP VARIANT PRO-10.
 RX PubMed=9783545;
 RA Yamada Y., Miyachi A., Goto J., Takagi Y., Okuzumi H., Kanematsu M.,
 RA Hase M., Takai H., Harada A., Ikeda K.;
 RT "Association of a polymorphism of the transforming growth factor-beta1
 RT gene with genetic susceptibility to osteoporosis in postmenopausal
 RT Japanese women.";
 RL J. Bone Miner. Res. 13:1569-1576(1998).
 RN [14]
 RP VARIANTS CED CYS-218; HIS-218 AND ARG-225.
 RX PubMed=10973241; DOI=10.1038/79128;
 RA Kinoshita A., Saito T., Tomita H., Makita Y., Yoshida K., Ghadami M.,
 RA Yamada K., Kondo S., Ikegawa S., Nishimura G., Fukushima Y.,
 RA Nakagomi T., Saito H., Sugimoto T., Kamegaya M., Hise K., Murray J.C.,
 RA Taniguchi N., Nikawa N., Yoshiura K.;
 RT "Domain-specific mutations in TGFbeta1 result in Camurati-Engelmann
 RT disease.";
 RL Nat. Genet. 26:19-20(2000).
 RN [15]
 RP VARIANTS CED HIS-81; CYS-218 AND ARG-225.
 RX PubMed=11062463; DOI=10.1038/81563;

RA Janssens K., Gershoni-Baruch R., Guanabens N., Magone N., Ralston S.,
 RA Bonduelle M., Lissens W., Van Maldergem L., Vanhoenacker F.,
 RA Verbruggen L., Van Hul W.;
 RT "Mutations in the gene encoding the latency-associated peptide of TGF-
 RT beta 1 cause Camurati-Engelmann disease.";
 RL Nat. Genet. 26:273-275(2000).
 RN [16]
 RP VARIANT PRO-10.
 RX PubMed=12202987; DOI=10.1007/s100380200069;
 RA Watanabe Y., Kinoshita A., Yamada T., Ohta T., Kishino T.,
 RA Matsumoto N., Iehikawa M., Nikawa N., Yoshiura K.;
 RT "A catalog of 106 single-nucleotide polymorphisms (SNPs) and 11 other
 RT types of variations in genes for transforming growth factor-beta1
 RT (TGF-beta1) and its signaling pathway.";
 RL J. Hum. Genet. 47:478-483(2002).
 RN [17]
 RP CHARACTERIZATION OF VARIANTS CED HIS-81; CYS-218; ASP-222 AND ARG-225.
 RX PubMed=12493741; DOI=10.1074/jbc.M208857200;
 RA Janssens K., ten Dijke P., Ralston S.H., Bergmann C., Van Hul W.;
 RT "Transforming growth factor-beta-1 mutations in Camurati-Engelmann
 RT disease lead to increased signaling by altering either activation or
 RT secretion of the mutant protein.";
 RL J. Biol. Chem. 278:7718-7724(2003).
 RN [18]
 RP CHARACTERIZATION OF VARIANT CYS-218.
 RX PubMed=12843182; DOI=10.1210/jc.2002-020564;
 RA McGowan N.W., Macpherson H., Janssens K., Van Hul W., Frith J.C.,
 RA Fraser W.D., Ralston S.H., Helfrich M.H.;
 RT "A mutation affecting the latency-associated peptide of TGFbeta1 in
 RT Camurati-Engelmann disease enhances osteoclast formation in vitro.";
 RL J. Clin. Endocrinol. Metab. 86:3521-3526(2003).
 CC -1- FUNCTION: Multifunctional peptide that controls proliferation,
 CC differentiation, and other functions in many cell types. Many
 CC cells synthesize TGF-beta 1 and essentially all of them have
 CC specific receptors for this peptide. TGF-beta 1 regulates the
 CC actions of many other peptide growth factors and determines a
 CC positive or negative direction of their effects. Play an important
 CC role in bone remodeling. It is a potent stimulator of
 CC osteoblastic bone formation, causing chemotaxis, proliferation and
 CC differentiation in committed osteoblasts (By similarity).
 CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
 CC covalently linked to a latency-associated peptide (LAP) homodimer.
 CC The inactive complex can contain a latent TGF-beta binding
 CC protein. The active form is a homodimer of mature TGF-beta 1;
 CC disulfide-linked.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Highly expressed in bone.
 CC -1- INDUCTION: Activated in vitro at pH below 3.5 and over 12.5.
 CC -1- PTM: Glycosylated (By similarity). The precursor is cleaved into
 CC mature TGF-beta 1 and LAP.
 CC -1- POLYMORPHISM: In post-menopausal Japanese women, the frequency of
 CC Leu-10 is higher in subjects with osteoporosis than in controls.
 CC -1- DISEASE: Defects in TGFBI are the cause of Camurati-Engelmann

Query Match 100.0%; Score 145; DB 1; Length 390;
 Best Local Similarity 100.0%; Pred. NO. 9.9e-13;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 HEPKGYANFCLGCPYIWSLDT 23
 Db 312 HEPKGYANFCLGCPYIWSLDT 334

RESULT 14
 TGF1_MOUSE STANDARD; PRT; 390 AA.
 AC P04202;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).
 GN Name=Tgfb1;
 OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=86168129; PubMed=3007454;
 CC Deynck R., Jarrett J.A., Chen E.Y., Goeddel D.V.;
 CC "The murine transforming growth factor-beta precursor";
 CC J. Biol. Chem. 261:4377-4379(1986).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN=BA1B/C;
 CC MEDLINE=96096545; PubMed=8522200; DOI=10.1016/0378-1119(95)00460-N;
 CC Guron C., Sudarshan C., Raghow R.;
 CC "Molecular organization of the gene encoding murine transforming
 CC growth factor beta 1.";
 CC Gene 165:325-326(1995).
 CC [3]
 CC SEQUENCE FROM N.A.
 CC STRAIN=C57BL/6, and NOD/LT; TISSUE=Spleen;
 CC Polrot L., Benoist C., Mathis D.;
 CC "Transforming growth factor-beta 1 sequence and expression: no
 CC difference between NOD/Lt and C57BL/6 mouse strains";
 CC Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
 CC [4]
 CC SEQUENCE FROM N.A.
 CC STRAIN=FVB/N; TISSUE=Mammary gland;
 CC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 CC Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 CC Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 CC Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 CC Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 CC Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 CC Stepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 CC Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 CC Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 CC Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 CC Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 CC Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 CC Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 CC Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 CC Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 CC Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 CC Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 CC Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;
 CC "Generation and initial analysis of more than 15,000 full-length human
 CC and mouse cDNA sequences";
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC [1-] FUNCTION: TGF-beta is a multifunctional peptide that control
 CC proliferation, differentiation, and other functions in many cell
 CC types. Many cells synthesize TGF-beta and essentially all of them
 CC have specific receptors for this peptide. TGF-beta regulates the
 CC actions of many other peptide growth factors and determines a
 CC positive or negative direction of their effects. Play an important
 CC role in bone remodelling. It is a potent stimulator of
 CC osteoblastic bone formation, causing chemotaxis, proliferation and
 CC differentiation in committed osteoblasts (by similarity).
 CC [1-] SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
 CC covalently linked to a latency-associated peptide (LAP) homodimer.
 CC The inactive complex can contain a latent TGF-beta binding
 CC protein. The active form is a homodimer of mature TGF-beta 1;
 CC disulfide-linked (by similarity).
 CC [1-] SUBCELLULAR LOCATION: Secreted.
 CC [1-] PTM: Glycosylation.
 CC [1-] SIMILARITY: Belongs to the TGF-beta family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>)

CC or send an email to license@isb-sib.ch.
 CC -----
 CC DR EMBL; M13177; AAA40423.1; -;
 CC DR EMBL; L42462; AAB00138.1; -;
 CC DR EMBL; L42456; AAB00138.1; JOINED.
 CC DR EMBL; L42457; AAB00138.1; JOINED.
 CC DR EMBL; L42458; AAB00138.1; JOINED.
 CC DR EMBL; L42459; AAB00138.1; JOINED.
 CC DR EMBL; L42460; AAB00138.1; JOINED.
 CC DR EMBL; L42461; AAB00138.1; JOINED.
 CC DR EMBL; AJ009862; CAA08900.1; -;
 CC DR EMBL; BC013738; AAH13738.1; -;
 CC DR PIR; A01396; WFMS2.
 CC DR HSSP; P01137; 1KLA.
 CC DR MGD; MGI.98725; Tgfb1.
 CC DR GO; GO:0005578; C:extracellular matrix; IDA.
 CC DR GO; GO:0006954; P:inflammatory response; IMP.
 CC DR GO; GO:0007515; P:lymph gland development; IMP.
 CC DR GO; GO:0008220; P:necrosis; IMP.
 CC DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
 CC DR GO; GO:0042127; P:regulation of cell proliferation; IDA.
 CC DR GO; GO:0016202; P:regulation of myogenesis; IDA.
 CC DR GO; GO:0042306; P:regulation of protein-nucleus import; IDA.
 CC DR GO; GO:0007179; P:transforming growth factor beta receptor si. .; IDA.
 CC DR Interpro; IPR002400; GF_cys_knot.
 CC DR Interpro; IPR003911; TGF_TGFB.
 CC DR Interpro; IPR001839; TGFB.
 CC DR Interpro; IPR001111; TGFB_N.
 CC DR Pfam; PF00019; TGF_beta_1.
 CC DR Pfam; PF00688; TGF_beta_propeptide; 1.
 CC DR PRINTS; PR00438; GFCYSKNOT.
 CC DR PRINTS; PR01423; TGFBRTA.
 CC DR ProDom; PD000357; TGFB_1.
 CC DR PROSITE; PS00250; TGF_BETA_1, 1.
 CC DR GlycoSite; Growth factor; Mitogen; Signal.
 CC KW SIGNAL 1 29
 CC FT PROPEP 30 278
 CC FT CHAIN 279 390
 CC FT DISULFID 285 294
 CC FT DISULFID 293 356
 CC FT DISULFID 322 387
 CC FT DISULFID 326 389
 CC FT DISULFID 355 355
 CC FT CARBOHYD 82 82
 CC FT CARBOHYD 136 136
 CC FT CARBOHYD 176 176
 CC FT SITE 244 246
 CC SQ SEQUENCE 390 AA; 44310 MW; 4381A51B71ID689E CQC64;
 CC Query Match 100.0%; Score 145; DB 13; Length 390;
 CC Best local similarity 100.0%; Pred. No. 9.9e-13;
 CC Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 HEPKGYANFCLGCPYIWSLDT 23
 CC DB 312 HEPKGYANFCLGCPYIWSLDT 334
 CC
 CC RESULT 15
 CC ID TGF1_PIG STANDARD; PRT; 390 AA.
 CC AC P07200; P08832;
 CC DT 01-APR-1988 (Rel. 07, Created)
 CC DT 01-APR-1988 (Rel. 07, Last sequence update)
 CC DT 05-JUL-2004 (Rel. 44, Last annotation update)
 CC DE Transforming growth factor beta 1 precursor (TGF-beta 1).
 CC GN Name=TGFBI; (Fig).
 CC OS Sus scrofa (Pig).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 CC OC NCBI_TaxID=9823;
 CC [1]
 CC SEQUENCE FROM N.A.

RC TISSUE=Ovary;
 RX MEDLINE=87174844; PubMed=3470708;
 RA Derynck R., Rhee L.;
 RT "Sequence of the porcine transforming growth factor-beta precursor";
 RL Nucleic Acids Res. 15:3187-3187(1987).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANT VAL-114.
 RC STRAIN=miniature swine;
 RX MEDLINE=89054010; PubMed=2461367;
 RA Kondarah P., van Obberghen-Schilling E., Ludwig R.L., Dhar R.,
 RA Sporn M.B., Roberts A.B.;
 RT "cDNA cloning of porcine transforming growth factor-beta 1 mRNAs.
 RT Evidence for alternate splicing and polyadenylation.";
 RL J. Biol. Chem. 263:18313-18317(1988).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANT VAL-114.
 RX MEDLINE=88335639; PubMed=3166520;
 RA Jakowlew S.B., Dillard P.J., Sporn M.B., Roberts A.B.;
 RT "Nucleotide sequence of chicken transforming growth factor-beta 1
 RT (TGF-beta 1).";
 RL Nucleic Acids Res. 16:8730-8730(1988).
 RN [4]
 RP SHOWS THAT REF.3 SEQUENCE IS FROM PIG.
 RA Jakowlew S.B.;
 RL Unpublished observations (MAR-1996).
 RN [5]
 RP SEQUENCE FROM N.A., AND VARIANT VAL-114.
 RA Wimmers K., Chomdel S., Ponsuksilli S., Schellander K.;
 RT "Polymorphism in the porcine transforming growth factor beta 1 gene.";
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 279-322.
 RX MEDLINE=87102890; PubMed=2879635; DOI=10.1016/0092-8674(87)90192-9;
 RA Cheifetz S., Weatherbee J.A., Tsang M.L.S., Anderson J.K., Mole J.E.,
 RA Lucas R., Massague J.;
 RT "The transforming growth factor-beta system, a complex pattern of
 RT cross-reactive ligands and receptors.";
 RL Cell 48:409-415(1987).
 CC -1- FUNCTION: TGF-beta is a multifunctional peptide that control
 CC proliferation, differentiation, and other functions in many cell
 CC types. Many cells synthesize TGF-beta and essentially all of them
 CC have specific receptors for this peptide. TGF-beta regulates a
 CC actions of many other peptide growth factors and determines a
 CC positive or negative direction of their effects. Play an important
 CC role in bone remodeling. It is a potent stimulator of
 CC osteoblastic bone formation, causing chemotaxis, proliferation and
 CC differentiation in committed osteoblasts (By similarity).
 CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
 CC covalently linked to a latency-associated peptide (LAP) homodimer.
 CC The inactive complex can contain a latent TGF-beta binding
 CC protein. The active form is a homodimer of mature TGF-beta 1;
 CC disulfide-linked (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1
 CC and LAP (By similarity).
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -1- CAUTION: Ref.3 sequence which was said to originate from chicken
 CC white leghorn, seems (Ref.4) to originate from pig.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Y00111; CAA68291.1; -;
 CC EMBL; M23703; AA64616.1; -;
 CC EMBL; X12373; CAA30933.1; -;
 CC EMBL; AF461808; AA57902.1; -;
 CC PIR; A27512; A27512.
 CC PIR; S01413; S01413.

DR HSSP; P01137; IKA.
 DR InterPro; IPR002400; GF_cysknot.
 DR InterPro; IPR003911; TGF_TGF.
 DR InterPro; IPR001839; TGF.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00018; TGF_beta_I.
 DR Pfam; PF00688; TGFb_propeptide_1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PRINTS; PR01423; TGFbeta.
 DR PRODOM; PD000357; TGFb_1.
 DR SMART; SMO0204; TGFb_1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Direct protein sequencing; Glycoprotein; Growth factor; Mitogen;
 KW Polymorphism; Signal.
 FT SIGNAL 1 29
 FT PROPEP 30 278 By similarity.
 FT CHAIN 279 390 Transforming growth factor beta 1.
 FT DISULFID 285 294 By similarity.
 FT DISULFID 293 356 By similarity.
 FT DISULFID 322 387 By similarity.
 FT DISULFID 326 389 By similarity.
 FT DISULFID 355 355 Interchain (By similarity).
 FT CARBOHYD 82 82 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 136 136 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 176 176 N-linked (GlcNAc...) (By similarity).
 FT SITE 244 246 Cell attachment site (potential).
 FT VARIANT 114 114 L -> V.
 FT CONFLICT 6 7 LR -> PG (in Ref. 3).
 FT CONFLICT 180 180 R -> G (in Ref. 3).
 FT CONFLICT 237 237 N -> NA (in Ref. 3).
 SQ SEQUENCE 390 AA; 44294 MW; A6E2C3659FC384E6 CRC64;

Query Match 100.0%; Score 145; DB 1; Length 390;
 Best Local Similarity 100.0%; Pred. No. 9.9e-13;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 HEPKGYANFCLGCPPIWISLDT 23
 Db 312 HEPKGYANFCLGCPPIWISLDT 334

Search completed: June 14, 2005, 15:51:07
 Job time : 123.962 secs